OM of: US-08-711-417C-165 to: SPTREMBL_19:*   out_format : pfs

Date: Aug 28, 2002 10:16 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/6228611/runat_28082002_100211_13637/app_query.fasta_1.1639
-DB=SPTREMBL_19 -QFMT=fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.000 -FGAPOP=10.000 -XGAPEXT=0.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=6228611_@CGN1_1_383 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-08-711-417C-165
Query length: 1551
Database: SPTREMBL_19:*
Database sequences: 562222
Database length: 172994929
Search time (sec): 172.940000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
sp_vertebrate:Q9PUG1	+	1964.00	2593.41	8.6e-137	482	! Q9pug1 ambystoma mexicanum (axo
sp_vertebrate:Q9I8W1	+	1810.00	2388.82	2.1e-125	500	! Q9i8w1 raja eglanteria. ikaros
sp_vertebrate:Q90XA3	+	1762.50	2325.41	6.7e-122	526	! Q90xa3 brachydanio rerio (zebra
sp_vertebrate:Q93581	+	1747.00	2304.56	9.4e-121	537	! Q93581 brachydanio rerio (zebra
sp_vertebrate:Q9I8V9	+	1402.50	1848.14	2.6e-95	513	! Q9i8v9 raja eglanteria. aiolos
sp_vertebrate:Q9I8W2	+	1395.50	1839.35	7.9e-95	522	! Q9i8w2 raja eglanteria. helios
sp_vertebrate:Q90XA2	+	1373.50	1811.34	3.5e-93	434	! Q90xa2 brachydanio rerio (zebra
sp_vertebrate:Q90WJ6	+	1351.50	1782.30	1.5e-91	428	! Q90wj6 seriola quinqueradiata (
sp_vertebrate:Q90W82	+	1341.50	1766.32	8.6e-91	563	! Q90w82 gallus gallus (chicken).
sp_human:Q9UKT9	+	1303.50	1716.93	5.4e-89	509	! Q9ukt9 homo sapiens (human). zi
sp_rodent:O08900	+	1302.00	1714.98	6.9e-88	507	! O08900 mus musculus (mouse). ai
sp_human:Q96JP3	+	1296.50	1706.90	1.8e-87	545	! Q96jp3 homo sapiens (human). ki
sp_rodent:Q9Z2Z2	+	1273.50	1676.68	8.9e-86	533	! Q9z2z2 mus musculus (mouse). ec
sp_vertebrate:Q9PU55	+	1260.00	1659.53	8.7e-85	494	! Q9pu55 gallus gallus (chicken).
sp_human:Q9H2S9	+	1252.50	1649.81	3.1e-84	483	! Q9h2s9 homo sapiens (human). zi
sp_vertebrate:Q90XA1	+	1220.50	1609.44	6.8e-82	392	! Q90xa1 brachydanio rerio (zebra
sp_vertebrate:Q90X58	+	1109.50	1460.24	1.1e-73	481	! Q90x58 ambystoma mexicanum (axo
sp_vertebrate:Q9I8U5	+	1007.50	1324.41	3.9e-66	507	! Q9i8u5 petromyzon marinus (sea
sp_vertebrate:P79751	+	996.50	1311.76	2.4e-65	417	! P79751 fugu rubripes (japanese
sp_vertebrate:O42244	+	806.00	1061.50	2.7e-51	328	! O42244 xenopus laevis (african
sp_vertebrate:Q90XA0	+	693.00	912.72	5.8e-43	294	! Q90xa0 brachydanio rerio (zebra
sp_human:Q96LD7	+	678.00	892.50	7.5e-42	304	! Q96ld7 homo sapiens (human). he
sp_vertebrate:Q9I8W0	+	676.50	893.89	8.8e-42	216	! Q9i8w0 raja eglanteria. eos (fi
sp_vertebrate:O13100	+	672.00	892.36	1.7e-41	138	! O13100 xenopus laevis/gilli. dr
sp_human:Q96NN3	+	448.50	593.32	5.8e-25	180	! Q96nn3 homo sapiens (human). co
sp_human:Q9H5V7	+	395.50	514.67	6.0e-21	419	! Q9h5v7 homo sapiens (human). co
sp_human:Q9H2T0	+	394.50	513.34	7.1e-21	419	! Q9h2t0 homo sapiens (human). zi
sp_invertebrate:Q95US1	+	365.50	467.93	1.2e-18	846	! Q95us1 locusta migratoria (mi
sp_invertebrate:Q95US0	+	349.00	451.02	1.7e-17	512	! Q95us0 locusta migratoria (mi
sp_human:Q9H9P0	+	341.50	442.09	6.0e-17	462	! Q9h9p0 homo sapiens (human). co
sp_human:Q9H7R5	+	333.50	428.68	2.5e-16	613	! Q9h7r5 homo sapiens (human). th
sp_invertebrate:Q95UR8	+	332.50	424.35	3.3e-16	830	! Q95ur8 schistocerca americana
sp_human:Q9Y2P0	+	331.50	426.94	3.5e-16	559	! Q9y2p0 homo sapiens (human). bo
sp_invertebrate:Q9N9D4	+	331.50	425.92	3.6e-16	620	! Q9n9d4 megaselia abdita. puta
sp_human:Q9NYW8	+	330.00	423.19	4.4e-16	714	! Q9nyw8 homo sapiens (human). rb
sp_human:Q96SE7	+	330.00	420.93	5.0e-16	839	! Q96se7 homo sapiens (human). zi
sp_human:Q9PDL1	+	324.50	414.70	1.2e-15	754	! Q9pdl1 homo sapiens (human). zi
sp_invertebrate:Q95UR9	+	324.00	418.34	1.4e-15	488	! Q95ur9 schistocerca americana
sp_human:Q96JH5	+	324.00	411.77	1.4e-15	948	! Q96jh5 homo sapiens (human). ki
sp_rodent:O70162	+	322.50	411.29	1.8e-15	814	! O70162 mus musculus (mouse). my
sp_human:Q9H6Z6	+	321.50	417.17	1.7e-15	393	! Q9h6z6 homo sapiens (human).
sp_human:Q96NJ6	+	320.00	412.75	2.4e-15	502	! Q96nj6 homo sapiens (human).
sp_human:Q9Y2A4	+	320.00	409.88	2.6e-15	671	! Q9y2a4 homo sapiens (human).
sp_human:O75850	+	317.00	408.74	4.0e-15	504	! O75850 homo sapiens (human).
sp_human:Q9P2J8	+	315.00	402.12	6.2e-15	752	! Q9p2j8 homo sapiens (human).

seq_name: sp_vertebrate:Q9PUG1

seq_documentation_block:
ID   Q9PUG1   PRELIMINARY;   PRT;   482 AA.
AC   Q9PUG1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TRANSCRIPTION FACTOR IKAROS.
OS   Ambystoma mexicanum (Axolotl).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC   Ambystoma.
OX   NCBI_TaxID=8296;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20093994; PubMed=10630298;
RA   Durand C., Charlemagne J., Fellah J.S.;
RT   "Structure and developmental expression of Ikaros in the Mexican
RT   axolotl.";
RL   Immunogenetics 50:336-343(1999).
DR   EMBL; AF186359; AAF01038.1; -.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   SMART; SM00355; ZnF_C2H2; 5.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
KW   DNA-binding; Metal-binding; zinc-finger.
SQ   SEQUENCE 482 AA; 53740 MW; 57351794 9D590F08 CRC64;

alignment_scores:
                Quality: 1964.00   Length: 517
                  Ratio: 4.454   Gaps: 5
     Percent Similarity: 85.300   Percent Identity: 72.534

alignment_block:
US-08-711-417C-165 x Q9PUG1

Align seg 1/1   to: Q9PUG1   from: 1   to: 482

1   ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGGAGGAAAG 50
     |||||||||||:::|||||||::||||||||||| |||||||:::|||||
1   MetAspAlaAspGluAlaGlnAspMetSerGlnValSerGlyAsnGlnSe 17

51   CCCCCCGTAAGCGATACTCCAGATGGAGGCGATGAGCCCATGCCGATCC 100
     |||||::|||||||||||||||||||||||||||||||||||:|||||
17   rSerProMetSerAspIleProGluAspGlyAspGluProMetProValP 34

101 CCGAGGACCTCTCCACCACCTCCGGGAGGACGAGCAGCAAAGCTCCAAGAGTGAC 150
     ||||:::||||||||||||||:::|||||::||||::|||||:::||||||
34   roGluAspLeuSerThrAsnSerGlyAlaGlnHisHisPheArgAsnGlu 50

151 AGAGTCGTGGCCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
     |||||||||:|||||||||||:::|||||||||||||::::||||||
51   LysAlaLeuAlaSerAsnValLysLeuGluAlaGlnSerAspAspGluAs 67

201 TGGGCTGCCTGTGAAATGAAATGGGGAAGAAATGTGCCGGAGGATTTACGAA 250
     |||:||||:::|||||||||||||||||||||||||||:|||||
67   nGlyHisAlaCysAspMetAsnGlyGluGluCysAlaAspLeuArgM 84

251 TGCTTGATGCCTCGGGAGGAGAAAATGAATGGCTCCCACAGGACCACAGGC 300
     |||:|||||||||||||||||||||||||||:|||||||||||| |||
84   etLeuAspAlaSerGlyGluLysMetAsnGlyLeuHisAspGlyProGly 100

301 AGCTCGGCTTTGTCGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACT 350
     |||:::|||||||||||||||||

us-08-711-417c-165.rspt

```
 101 SerLysAlaLeuSerGlyValGly.............................. 108
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 351 AAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400

 108 .................................................. 108

 401 TTCCAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC 450
     ||||||||||||||||||||||||||||||||||||||||
 109 .........GlyGluArgProPheGlnCysAsnGlnCys 118

 109 .........GlyGluArgProPheGlnCysAsnGlnCys 118

 451 GGGGCCTCATTCACCCAGAAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
     ||||||||||||||||||||||||||||||||||||||
 119 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 135

 501 TTCCGGGGAGAAGCCCTTCAAATGCCACCTGTGCAACTACGGCCTGCCGCC 550
     ||||||||||||||||||||||||||||||||||||||
 135 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 152

 551 GGAGGACGGCCCTCACTGGCCACCTGAGGACCGACTCCGTTGTAAACCT 600
     ||||||||||||||||||||||||||||||||||||||
 152 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 168

 601 CACAAATGTGATATTGTGGCCGAAGCTATAAACAGCGACGTCTTTAGA 650
     |||||||||||||||||||||||||||:::||||||||
 169 HisLysCysGlyTyrTyrCysGlyArgSerTyrLysGlnArgSerLeuGl 185

 651 GGAACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGG 700
     ||||:|||| ||||||||||||||||:::||||||||||
 185 uGluHisLysGluArgCysHisAsnTyrLeuGlnSerMetGlyLeuProG 202

 701 GCACACTGTACCCAGTCATTAAAGAAGAAAACTAAGCACAGTGAAATGGCA 750
     ||:::||||| ||||||||||||||||:::: |||||
 202 lyAsnLeuTyrAlaLeuValLysGluGluThrAsnProSerAspMetPro 218

 751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTGCTGGACAGACT 800
     |||||||||||||||||||||||||||:::||||||||
 219 GluAspLeuCysLysIleGlySerGlyArgSerLeuMetLeuAspArgLe 235

 801 AGCAAGTAATGCTGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850
     ||||||||||||||||||||||||||||||:::||||
 235 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheValG 252

 851 GGGACAAGGGCCTGCTCCGACACGCCCTACGACAGTGCCACG...TACGAG 897
     |:::|||  ||||||||| |||||:::::|||  ||||||
 252 lyGluLysArgLeuSerAspHisProPheAspAlaSerThrProTyrGlu 268

 898 AAGGAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAA 947
     ||||||||||||||| ||||||||:::|||||||||||||
 269 LysGluAsnGluMetMetGlnThrGlnValIleAspGlnAlaIleAsnAs 285

 948 CGCCATCAACTACCTGGGGCCGAGTCCCTGGCCGCCGGTGCGACAGC 997
     |||||||||||||||||||||||||||||||||||||
 285 nAlaIleSerTyrLeuGlyLeuGlyLeuProLeuValGlnThrP 302

 998 CCCCGGGGGTTCCGAGGTGGTCCCCGTCATCAGCCCGATGTACCAGCTG 1047
     ||||||| |||:::|  |||||||||||||||||||||
 302 roProGlyCysSerAsp........ValIleSerSerMetTyrGlnLeu 315

1048 CACAGG...CGCTCGGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGA 1094
     |::::|| ||||||||||||||||::::||||| :::||
 316 GlnLysProGlnSerAspGlyGlnProArgAsnAsnHisMetProHisAs 332

1095 CAGCGCCCGTGGAGTACCCTGCTCTCCACAAGGCCAAGTTGGTGCCCT 1144
     |:::||| || |||||||||||||||| :||  |||||
 332 pGlyAlaGlyGluAsnLeuLeuLeuLeuLeuLeuSerLysAlaLysSerS 349

1145 CGGAGGCGCGAGGCGTCCCCGACCAACAGCTGCCACGGACTCCACGGACACC 1194
     ||||||:::  |||||||||||||||||||||||||||
 349 erGluArgAspProSerProSerAsnSerLeuGlnAspSerThrAspThr 365

1195 GAGAGCAACAACGAGGAGCCGCCAGCCGCGCGTCTTATCTACCTGACCAACCA 1244
     ||:::|||||||  |||||||||||||||||||||||
 366 GluSerAsnAsnGluGlu...ArgGlyGlyLeuIleTyrLeuThrAsnHi 381
```

```
1245 CATCGCCCGACGCGGCAACGCGTGTCGCCTCAAGAGGAGCACCGCGCCT 1294
     |||||||        ||:::  :::::          ||| |
 381 sIleAlaProHisLeuArgAsnGlyLeuSerAlaLysAspLeuArgProT 398

1295 ACGACCTGCTGCGCGCCGCCTCCGAGAACTCGCAGGACGGCCTCCGGTG 1344
     ||||:::||||||||||:::|||||||||:::    :::||:|||
 398 yrAspMetLeuArgAlaGlyAlaAspAsnSerGlnGlnProPheLysVal 414

1345 GTCAGCACCAGCGGGAGCAGATGAAGTGTACAAGTGCAACACTGCCG 1394
     ||||:::||||||      :::::||||||||||     ||||
 415 ValSerSerSerGlyGlyProLeuArgMetTyrLysGluProCysAr 431

1395 GGTGCTCTTCCTGATCACGTCATGTCAACATCCACATGGCTGCCACG 1444
     |||||||||||||||||||||||||||||||||||||||||||
 431 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 448

1445 GCTTCCGTGATCCTTTTGAGTGCAACATGTGCGCTACCACAGCCAGGAC 1494
     ||||||||||||||||||||||||||||||:::  ||||||
 448 lyPheArgAspProPheGluCysAsnMetCysGlyTyrGlnCysGlnAsp 464

1495 CGGTACGAGTTCTCGTCGCCACATAACGCGAGGGGAGCACCGCTTCCACAT 1544
     ||||||||||||||||||||||||||||||||||||||
 465 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArgPheHisMe 481

1545 G 1545

 481 t 481
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seq_name: sp_vertebrate:Q9I8W1

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alignment_scores:
  Quality: 1810.00   Length: 530
  Ratio: 4.132   Gaps: 10
Percent Similarity: 82.642   Percent Identity: 65.849

alignment_block:
US-08-711-417C-165 x Q9I8W1

Align seg 1/1 to: Q9I8W1   from: 1 to: 500

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 1 ATGGATGCTGACGAGGGTCAAGACATGTCTTTTCATCAGG......... 42
   |::::::::::||:::||||||||::::|||
 1 MetGluThrGluGluGlnAspIleSerGlnGlnLeuSerGlyGluThrGl 17
```

```
43 ....AAGGAAAGCCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGC 88
   |||||||:::  |||  |||:::::     |||
17 ySerLysGluAlaLeuSerIleIleAspGlnProGluGln...LeuGluG 33

89 CCATGCGATCCCGCAGGACCTTCCACCACTTCGGGAGGACAGCAAAGC 138
   |||||||||||||||:||||||::  ||:::|||||||::  :::
33 lnMetProValProGluAspLeuSerThrSerAlaGlyGlyLysIleAsn 49

139 TCCAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAG 188
   :::|||||||:::||:||||||||||:::||||||:::|||||||  ||
50 LeuGlnGlyTyrAspLysValIleAlaAsnSerIleLysValGluThrProSe 66

189 TGATGAAGAGAATGGGCTGCCTGTGAAATGAATGGGGAAGAATGTGCGG 238
   ||||||||||||||:::  |||||||:::|||||||||:::||||||
66 rAspGluGluAsnGlyArgAlaCysAspThrAsnGlyGluAspCysAlaG 83

239 AGGATTTACGAAGCTTGATGCCTGGGAGAGACAAAATGAATGGCTCCCAC 288
   |||||||||||||:||||||||||:::|||||||||   ||:::|||||||
83 luAspLeuArgMetIleAspThrSerGlyThrLysLeuAsnGlyProHis 99

289 AGGGACCAAGGCAGCTCCGCTTTGTCGGGAGTTGGAGGCATTCGACTTCC 338
   :::  |||||||||:||:::||||||||||||||||:::||||||||||||
100 AsnGlyGlnGlyLysAlaPheSerGlyLysValGlyValGlyIleArgLeuPr 116

339 TAACGGAAAACTAAAGTGTGATATCTTGTGGGATCATTTGCATCGGGCCCA 388
   |||
116 oAsn..................................... 117

389 ATGTGCTCATGTGTTCACAAAAGAAGCCACACTCGAGAACGGCCCCTTCCAG 438
                        ||||||||||||||||||||||||||||
118 .....................GlyGluArgProPheGln 123

439 TGCAAATCAGTGCGGGGCCTCATTCACCCGGAGAGGGCAACCTGCTCCGGCA 488
   ||||||||:||:||||||||||||||||||||||||||||||||||||||
124 CysSerGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHi 140

489 CATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACT 538
   |||:|||||||||||||||||||||||||||||||||||||||||||||
140 sIleLysLeuHisSerGlyGluLysProPheLysCysHisLeuCysAsnT 157

539 ACGCCTGCCGCGAGGAGACGCCCTCACTGCCACCTGAGGACGCCACTCC 588
   ||||||||||||||||||:::||||||||||||||||||||||||||
157 yrAlaCysArgArgArgAspAlaLeuSerGlyHisLeuArgThrHisSer 173

589 GTTGGTAAACCTCACAAATGTGATATTGTGCCGAAGCTATAAACAGCG 638
   |||||||||||||||:::|||||||||||||||||||||||||||
174 ValGlyLysProHisLysCysAspIleValArgSerTyrLysGlnAr 190

639 AACGTCTTTAGAGGAACAATAAAGAGCGCTGCCACAACTACTTGGAAAGCA 688
   |::||||||||||||||:::|||||||||||||||||||||||||
190 gSerSerLeuGluGluHisLysLysGluArgCysHisAsnTyrLeuGlnThrM 207

689 TGGGCCTTCCGGGCACACTGTACCCAGTCATTAAAGAAGAAAACTAAGCAC 738
   ||||||  ||  :::||  |||  |||:::|||
207 etGlyLeuHisGlyGlyIleTyrSerVal...LysGluSerLysSer 222

739 AGTGAAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTCGT 788
   ||||::||||||  ||||||||:::|||||||||||||:::||
223 HisGluLeuAlaGluGlyAlaSerLysIleLeuGlySerGluArgAlaMetVa 239

789 GCTGGACAGACTAGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCCTC 838
   |||||||||||||||||||||||||||:::||||||||||||||||||
239 lLeuAspPArgGluLeuAlaSerAsnValAlaLysSerArgLysSerMetProG 256

839 AGAAATTTCTTGGGACAAG.........GGCCTGTCCGACACGCCC 876
   |||||||||:::|||          ||:::||||
256 lnLysPheValGlyGluLysThrValGlnLeuGlyIleLeuSerGluLeuGln 272

877 TACGAC...AGTGCCACGTACGAGAAGGAGAACGAAATGATGAAGTCCCA 923
   |||||||          ||||||||:::|||||||:::||
273 CysAspAlaAsnSerAsnTyrGluLysGluSerGlnMetMetGlnThrHi 289
```

```
924 CGTGATGGACCAAGCCATCAACAACGCCATCAACTACCTGGGGCCGAGT 973
   |||:::||||||||||||||||||||||||||||||||||||||||||
289 sValLeuAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGlyAlaGlus 306

974 CCCTGCGCCCGCTGGTGCAGACGCCCCGGGCGGTTCCGAGTGGTCCCG 1023
   ||||||||||||||||||||||||||||||||||||||||::::|||
306 erLeuArgProLeuValGlnThrProAlaGlySerSerGluValIlePro 322

1024 GTCATCAGCCCGATGTACCAGCTG.......CACAGGCGGCTCGGAGGG 1064
    ||||||||||||| ||||||  ::        ||  |||:::|||||
323 ValLeuSerAsnMetTyrProMetGlnIleThrHisSerAspThrHisGl 339

1065 CACCCCGGCGCTCCAACCACTCGGCCCAGGACAGCGCCCTGGAGTACCTGC 1114
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339 yHisProAsnCys...AlaThrIleGlnAsnGlyAlaValGluAsnLeuM 355

1115 TGCTGCTCTCCAAGGCCAAGTTGGTGCCCTGGAGCGCCGAGCGTCCCCG 1164
    ::||||:||||||||||||||||||||||||||||||||||||:||||
355 etLeuIleSerLysAlaLysSerGlnThrSerGluArgGluProSerPro 371

1165 AGCAACAGCTGCCAAGACTCCACGGACACCGAGACAACAACGAGGAGACA 1214
    ||||||||||  ||||||||||||:::||||||||||||||||||||||
372 SerAsnSerCysProAspSerThrAspThrGluSerAsnAsnGluGlu.. 387

1215 GCGCAGCGGTCTTATCTACCTGACCAACCACATCGCCCGACGGCGCGCAAC 1264
    |||||||||||:::|||||||||||||||:::|||    :::||:::|
388 .ArgAsnAsnLeuIleTyrLeuThrAsnHisValAlaProGlnAlaArgA 404

1265 GC......GTGTGCTCCAAGGAGGAGGAGCACCCGCCTACGACCTGTGCGC 1308
    ::                    ||||||||||||||||||:::|||||
404 snGlyLeuProLeuIleLysGluAspGlnArgSerTyrAspLeuMetArg 420

1309 GCCGCCTTCCGAGAACTCGCAGGACGCGCTCCGCGTCCTGGTCAGCACCAGCGG 1358
    :::||  :::||    :::||||||||||||:::|||||||||:::|||
421 SerGlyMetGluProAsnGlnGluIleLeuIleLysValValSerAlaAspGl 437

1359 GGAGCAGATGAAGGTGACAAGTGCCAAACTGCCGGGTGCTCTTCCTGG 1408
    |||||||||||||||||||||||||||||||||||||||||||||
437 yGluHisMetLysValTyrLysCysGluHisCysSargValLeuPheLeuA 454

1409 ATCACGTCATGTACACCACATCCCACATGGGTGCCACCGGCTTCCGTGATCCT 1458
    |||||||||:::|||||||||||||||||||||||||||||||||||
454 spHisValMetPheThrIleHisMetGlyCysHisLisGlyPheArgAspPro 470

1459 TTTGAGTGCAACATGTGCGGCTACCACAGCCAGGACCGGTACGAGTTCTC 1508
    ||||||||||||||||||||||||||||||||||||||||||||:||
471 PheGluCysAsnMetCysGlyTyrArgSerGlnAspArgTyrGluPheSe 487

1509 GTCGCACATAACGCCAGGGGAGCACCGCTTCCACATGAGC 1548
    |||||||||||:::||||||||||||||||||  :::
487 rSerHisIleThrArgGlyGluHisCysHisCysTyrHisMetAsn 500
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seq_name: sp_vertebrate:Q90XA3

us-08-711-417c-165.rspt

Wed Aug 28 10:05:27 2002

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DR   EMBL; AF416370; AAL11906.1; -
SQ   SEQUENCE   526 AA;  57510 MW;  OEBA4C49AAAF623E CRC64;

alignment_scores:
     Quality:  1762.50      Length:     535
     Ratio:       3.874      Gaps:        12
Percent Similarity:  85.047   Percent Identity:  63.738

alignment_block:
US-08-711-417C-165 x Q90XA3   ..

Align seg 1/1   to: Q90XA3   from: 1   to: 526


   1 ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGAAGGAAAG    50
     |||::::::||::||::::|||||              :::||||:::||
   1 MetGluThrGluGluAlaGlnGluMetSerGlnIleThrGlyArgAspSe  17

  51 CCCC...CCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGA  97
     ||||      :::::::   |||||||||||||||
  17 rProMetAsnAlaAsnGluGlyGlyGluAspGlnAspGluAlaMetProV  34

  98 TCCCCGGAGCCTTCCACCACTTCGGGAGGACAGCAAAGCTCCAAGAGT  147
     :||||||||||||||||::::|||  |||::||||||||
  34 alProGluAspLeuSerAlaSerThrGlyLeuGlnHisAsnAsnArgThr  50

 148 GACAGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGA  197
     ||::  :::|||  |||:||||||||||||||::||||
  51 AspLysProLeuAlaCysAsnIleLysValGluAlaArgSerAspGluGl  67

 198 GAATGGGCGTGCCTGTGAAATGAATGGG......GAAGAATGT...GCGG  238
     ||||||  ::||||||||||||||         ||||            ||||
  67 uAsnGlyLeuSerCysGluMetAsnGlyGluAlaGluCysAlaAlaG      84

 239 AGGATTTACGAAATGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCAC  288
     |||||||||||||::||||||  ||||:::||||||||||
  84 luAspLeuArgIleLeuAspGlySerGlyAlaLysValAsnGlySerHis  100

 289 AGG.......GACCAAGGCAGCTCGGCTTGTCGGGAGTTGGAGGCATTCG  332
     |||::     :::|||          ||||||||||||||
 101 AlaGlyProAspSerLysProAlaAlaTyrProThrAlaGlyIleArg    117

 333 ACTTCCTAACGGAAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCG  382
     ||||||||||||||||||||||||||||::::||||||
 117 gLeuProAsnGlyLysLeuLysCysAspIleCysGlyIleIleCysIleG  134

 383 GGCCCAATGTGCTCATGGTTCACAAAAGAAGCCACACTGGAGAACGGCCC  432
     |||||||||||||||||||||||||||||||||||||||||||||
 134 lyProAsnValLeuMetValHisLysArgSerHisThrGlyGluArgPro  150

 433 TTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAACCTGCT  482
     ||||||||||||||||||||||||||||||||||||||||
 151 PheGlnCysAsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLe  167

 483 CCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCT  532
     |||||||||||||||||||||||||||||||||||||::||||||
 167 uArgHisIleLysLeuHisSerGlyGluLysProPheLysCysHisLeuC  184

 533 GCAACTACGCCTGCGCCGAGGGACCCCTCACTGGCCACCTGAGGACG    582
     |||||||||||||||||||||||||||||||||||||
 184 ysAsnTyrAlaCysAlaArgArgAspAlaLeuThrGlyHisLeuArgThr  200

 583 CACTCCGTTGGTAAACCTCACAAATGTGATATTGTGCCGAAGCTATAA   632
     |||||||::|||||||||||||||||||
 201 HisSerValGlyLysProHisLysCysAspIleCysGlyLysArgTyrLy  217

 633 ACACGGGAAGTCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACTTGG  682
     |||||||:::|||||||||||||||||||||||
 217 sGlnArgSerLeuGluGluHisLysLysGluArgCysHisAsnTyrLeuG  234

 683 AAAGCATGGGCCTTCCGGACCACTGTACCCAGTCATTAAAGAAGAAACT   732
     ::   ||||||||||::::|||||        :::||||||||||:::
 234 lnCysMetGlyLeuGlnAsnSerIleTyr...ThrValLysGluGluAsn  249

 733 AAGCCACAGTGAAATGGCAGAAGAGACCTGTGCAAGATGATAGGATCAGAGAGATC  782
     ::::::|||::|     ||||:::                  :::
 250 SerGlnAsnGluGlnArgGluAspPMet......ProAlaSerGluArgAl  264

 783 TCTCGTGCTGGACAGACTAGCAAGTAATGTCGCCAAACGTAAGAGCTCTA  832
     :||||||:::::::::||||::||||||||||||||||
 264 aLeuValLeuAspArgIleAlaAsnAsnValAlaLysArgLysSerSerM  281

 833 TGGCTCAGAAATTCTTGGGACAAGGGGCCTTCCGACACGCCCTACGAC   882
     |||||||||||::|||::||:||  ||||||||       :::::
 281 etProGlnArgPheValGlyGluAsnArgLeuSerPheGlu          297

 883 AGTGCCACGTACGAGAGGAGAACGAAATGATGAAGTCCCACGTGATGGA   932
     |||::::::                           |||::::::
 298 SerGlySer..........GlyGluLeuMetGlnProHisValIleAs   310

 933 CCAAGCCATCAACAACGGCCATCAACTACCTGGGGCGGTCCTGGCC     982
     ||||||||||||::::::|||||||||||||||||||||||||
 310 pGlnAlaIleAsnSerAlaIleSerTyrLeuGlyAlaGluSerLeuArgP  327

 983 CGCTGGTGCAGACGCCCCCCGGCGCGGTTCCGAGGTGGTCCCGGTCATCAGC  1032
     ||||||||||||    :::::::::||||||||||        |||::||||
 327 roLeuValGlnThrSerProGlyGlySerAlaAspMet......ValValSer  341

1033 CCGATGTACCAGCTGCACAGGCCGTCGGAGGGCACCCCGGCTCCACCA   1082
     ||||||         :::  :::||||||||||||          :::::
 342 ProLeuTyrAsnLeuHis...LysSerGlnThrAlaGluGluValAsnGlyVa  357

1083 CTCGGCCCAGGACAGCGCCGTGGAGTACCTGCTGCTCCAAGGCCA    1132
     ||||||||::||||||||||||||||||||:::||||||||||:::||||
 357 lSerAlaLysAspSerAlaIleAlaGluHisLeuLeuLeuSerLysSerL  374

1133 AGTTGGTGCCCTCGGAGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGAC  1182
     |||||||||||::||||||||||||||||||||
 374 ysSerAlaSerValAspLysValAspGlySerProSerProSerGlyGlnAsp  390

1183 TCCACGGCACACCGAGCAACAACAGGAGCAGCCGCAGC..........  1221
     ||||||||||||||||||||:::  ||             :::
 391 SerThrAspThrGluSerAsnGluGluArgSerAlaGlyValSerGl    407

1222 ..........GGTCTTATCTACCTGACCAACCACCATCGCCCGAC    1255
               ||||||||||||||||||||||||:::||||||
 407 yThrAlaAlaThrGlyGlyLeuIleTyrLeuThrAsnHisMetAlaProG  424

1256 GCCGCAACGCGTGTCGCTC..........AAGGAGGAGCACCGGCGCC   1293
     :::::    ::|||               ::|||||||||||||||
 424 lyMetArgAsnGlyGlyLeuProGlyValValLysGluGlnGlnArgHis  440

1294 TACGACCTGCTGCGCGGCGCC..........TCCGAGAACTCGCAGGA   1331
     :::::: ||||||||||             |||      ::::::
 441 PheGluAlaLeuArgAlaAlaGlyMetAspLeuSerIleAlaSerSerGl  457

1332 CGCGGCTCCGCGTGGTCAGCACCACGGGGAGCAGATGAAGGTGTACAAGT  1381
     |||||||||||||    ::|||||:::|||||||||||||
 457 uGlyPheLysValLeuSerGlyAspGlyGluLeuGluArgAlaTyrArgC  474

1382 GCGAACACTGCGGGTGCTCTTCCTGGATCACGTCATGTACCATCCAC   1431
     ||  |||||||||||||||||||||||||||||||||
 474 ysIleHisCysArgValLeuProPheLeuAspHisValMetTyrThrIleHis  490

1432 ATGGGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTA  1481
     |||||||||||||||||||::||||||||||||||||
 491 MetGlyCysHisGlyPheArgAspProPheGluCysAsnLeuCysGlyTy  507

1482 CCACAGCCAGGACCGGTACGAGTTCTCCGCACATAACGCGAGGGAGC    1531
     |:::|||||||||||||||||||||||||||||||
 507 rArgSerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluH  524

1532 ACCGC  1536
     |||||
 524 isArg  525
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seq_name: sp_vertebrate:O93581

seq_documentation_block:
ID   O93581          PRELIMINARY;        PRT;   537 AA.
AC   O93581;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   IKAROS.
GN   IKAROS.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RA   Amemiya C., Kawasaki H.;
RT   "Characterization of zebrafish ikaros, a gene necessary for
RT   differentiation of the immune system.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR   EMBL; AF092175; AAC61763.1; -.
DR   ZFIN; ZDB-GENE-980526-304; ikaros.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 5.
DR   PRINTS; PR00048; ZINCFINGER.
DR   SMART; SM00355; ZnF_C2H2; 6.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ   SEQUENCE   537 AA;   58865 MW;  3BF047938CF38A37 CRC64;

alignment_scores:
          Quality:  1747.00         Length:     546
            Ratio:     3.840           Gaps:      13
Percent Similarity:   83.333    Percent Identity:  62.454

alignment_block:
US-08-711-417c-165 x O93581

Align seg 1/1  to: O93581  from: 1  to: 537

   1 ATGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGGAAGGAAAG  50
     ::|||||||::|||:||:||||||        ::|||:::::::|||
   1 MetGluThrGlyAlaGlnGluMetSerGlnIleThrGlyArgAspSe  17

  51 CCCC...CCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGA  97
     ||||      ::::::::      ::::: |||||  ||||::
  17 rProMetAsnAlaAsnGluGlyGlyGluAspGlnAspGluAlaMetProV  34

  98 TCCCCGAGGACCCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGT  147
     ::||||||||||||:::::::|||        |||::::::::::||||
  34 alProGluAspLeuSerAlaSerThrGlyLeuGlnHisAsnAsnArgThr  50

 148 GACAGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGA  197
     ||:::   ::|||    ||::|||:|||||||||::::||||||||||
  51 AspLysProLeuAlaCysAsnIleLysValGluAlaArgSerAspGluGl  67

 198 GAATGGGCGTGCCTGTGAAATGAATGGG.....GAAGAATGT...GCGG  238
     ||||||     ::|||||:|||||::::::     ||||       ||||
  67 uAsnGlyLeuSerCysGluMetAsnGlyGluAlaGluGluCysAlaAlaG  84

 239 AGGATTTACGAATGCTTGATGCCTCCGGGAGAGAAATGAATGGCTCCCAC  288
     ||||||||||::||||||:::||||||   :||||||||||||||||||
  84 luAsnGlyIleLeuAspProSerGlyGlyValGluLysValAsnGlySerHis  100

 289 AGG.......GACCAAGGCAGCTCGGCTTTGTCGGGAGTTGGAGGCATTCG  332
     |||:::     :::|||  ||| :::||||||||||||||||||||||
```

```
101 AlaGlyProAspSerLysProAlaAlaTyrProThrAlaGlyGlyIleAr  117
    |||||||||||||||||||||||||||||||||||:::||||:|
333 ACTTCCTAACGCAGAAACTAAAGTGTGATATCTGTGGGATCATTGCATCG  382
    ||||||||||||||||||||||||||||||||:::||||:|:::||||
117 gLeuProAsnGlyLysLeuLysCysAspIleCysGlyIleValCysIleG  134

383 GGCCCAATGTGCTCATGGTTCACAAAAGAAGCCACACT..........  420
    ||||||||||||||||||||||||||||||||||||||
134 lyProAsnValLeuMetValHisLysArgSerHisThrGluArgLys  150

421 ............GGAGAACGGCCCTTCCAGTGCAATCAGTG  449
                ||||||||||||||||||||||||||||
151 SerValLeuGluGlnLysGlyGluArgProPheGlnCysAsnGlnCy  167

450 CGGGGCCTCATTCACCCAGAAGGCAACCTGCTCCGGCACATCAAGCTGC  499
    ||||||||||||||||||||||||||||||||||||||||||||||||
167 sGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuH  184

500 ATTCCGGGAGAGCCCTTCAAATGCCACCTGCAACTAGGCCTGCCGC  549
    |||||||||||||||||||||||||||||||||||||||||||||||
184 isSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArg  200

550 CGGAGGGACGCCCTCACTGGCCACCTGAGGACGCCACTCCGTTGGTAAACC  599
    |||||||||||||||||||||||||||||||||||||||||||||||||
201 ArgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPr  217

600 TCACAAATGTGGATATTGTGGCGAAGCTATAAACAGCGAACGTCTTTAG  649
    |||||||:::||||||||||||||||||||||||::::||||||||||
217 oHisLysCysAlaTyrCysGlyLysArgSerTyrLysGlnArgSerLeuG  234

650 AGGAACACATAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCG  699
    ||||||||||||||||||||||||||||::::        ||||||||
234 luGluHisLysGluArgCysHisAsnTyrLeuGlnCysMetGlyLeuGln  250

700 GGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGC  749
    :::::::||||     :::::||||||||||||||::||:::::::||:
251 AsnSerIleTyr....ThrValLysGluGlnAsnSerGlnAsnGluGlnAr  266

750 AGAAGACCTGTGCAAGATAGGATCAGAGAGATCTCGTGCTGGACAGAC  799
    ||||||:::          :::||||||||||||::||||||||||||
266 gGluAspMet......ProAlaSerGluArgAlaLeuValLeuAspArgI  281

800 TAGCAAGTAAATGTCGCCAAACGTAAGAGCTCTATGCCTCAGAAATTTCTT  849
    ::|||:||||:::|:::|||||||||||::||||||||||||::||:::
281 leAlaAsnAsnValAlaLysArgLysSerSerMetProGlnArgPheVal  297

850 GGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAA  899
    ||:::|||    :::||||||||||||::||||||||||||||||||||
298 GlyGluAsnArgLeuSerGluLeuSerPheGluSerGlySer........  311

900 GGAGAACGAAATGATGAAGTCCCACGTGATGACCAAGCCATCAACAACG  949
    |||||:::||:::      ||||||||||||||||||||||||::::
312 ....GlyGluLeuMetGlnProHisValIleAspGlnIleAlaIleAsnSerA  327

950 CCATCAACTACCTGGGGCCGAGTCCCTGCGCCCGCTGGTCCAGACGCCC  999
    ||||||||||||||||||||||||||||||||||||||||||||||||
327 laIleSerTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrSer  343

1000 CCGGGCGGTTCCGAGGTGTCCCGGTCATCAGCCCGATGTACCAGCTGCA  1049
     ||||||||||||:::||:||||||||    :::||:::||:::||||
344 ProGlySerAlaAspMet......ValValSerProLeuTyrAsnLeuHi  358

1050 CAGGCGCTCGGAGGGCACCCGGCTCCAACCACTCGGCCCAGGACAGCG  1099
     :::|||  :::::::     :::::      ||||||||||||||||
358 s....LysSerGlnThrAlaGluLysAsnGlyValSerAlaLysAspSerA  374

1100 CCGTGGAGTACCTGCTCGTCCTCCAAGGCAAGTTGGTGCCCTCGGAG  1149
     ||:::|||||||||||||||:::||||||||    :::||||||||
374 laAlaGluHisLeuLeuLeuLeuSerLysSerLysSerAlaSerValAsp  390

1150 CGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCACGGACACCGAGAG  1199
     :::::||||||||     |||   :::||||||||||||||||||||
391 LysAspGlySerProSerProSerGlyGlnAspSerThrAspThrGluSe  407
```

Wed Aug 28 10:05:27 2002

Align seg 1/1   to: Q9I8V9   from: 1 to: 513

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   1 ATGGATGCTGACCAGGTCAAGACATGTCT....................TT    32
     |||  :::::::::::::::::||::|||                     ::  :
   1 MetValThrGluAspAsnGlnGlnIleSerHisProGluAlaSerPheLe    17

  33 CTCATCAGGGAAGGAAAGCCCCCTGTAAGCGATACTCCAGATGAGGGCG   82
     ||||||||||||||||||||:::||:||||::||||:|||||
  17 uSerAspAlaGluThrValProThrValThrAspAlaProAsp.......   31

  83 ATGAGCCCATGCCATCCCGAGGACCTCTCCACCACCTCGGGAGGACACAG  132
     ::||||||| |||||||||:|||||    |||||||       |||
  32 ..........LeuProGluLysIleAsnValAlaAspAlaValGln    43

 133 CAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAATGTT...........  171
     ::|        |  :::::          :::::::::|||
  44 GluProIleLysGlnLeuSerThrAsnGlyValThrAlaGlyVal    60

 172 ........AAAGTAGAGACTCAGATGAT......................  196
     ::       :::||:|                             :::
  60 aValArgValTyrAspGluSerGluAlaAlaLeuAspLeuSerAspG    77

 197 AGAATGGGCGTGCCTGTGAAATGAATGGGGAAGAAATGTGCGGAGGATTA  246
     ||::::|| ||| ::|||  :|::||  :::||::
  77 luGlyCysHisAlaGlyGluTyrGlyThrAsnSerSerCysLeu   93

 247 CGAATGCTTGATGCCTCGGAGGAGAAAATGAATGGCTCCCAC...AGGGA  293
     |||||||||||||||:::||||||||||||
  94 ..........ValGluAsnGluAspTyrAsnGlyAspHisPheSerAla  106

 294 CCAAGGCAGCTTCGGCTTGTCGGAGGTTGGAGGCATTGGACTTCCTAACG  343
     :||:  ||||:||||                 |||||||
 106 nGlnProSerThrAla..........AspGlyIleArgAlaSerAsnG  119

 344 GAAAACTAAAGTGTGATATCTGGGATCATTTGATCGGGCCCAATGTG  393
     ||||||   |||||||||||||||:::   ||:::||||||||||
 119 lyLysLeuThrCysAspIleCysAspIleCysGlyLeuSerCysValGlyProAsnVal  135

 394 CTCATGGTTCACAAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAA  443
     ||||||||||::::||||||||||||||||||||||||||::||||
 136 LeuMetValHisLysArgSerHisThrGlyGluArgProPheHisCysAs  152

 444 TCAGTGCGGGCGCTCATTCACCCAGAGAGGGCAACCTGCTCCGGCACATCA  493
     |||||||||||||||||||||:::||||||||||||||||:::||:
 152 nGlnCysGlyAlaSerPheThrGlnArgGlyAsnLeuLeuArgHisValL  169

 494 AGTCGCATTCCGGGAGAAGCCCTTCAAATGCCACCTTCGCAACTACGCC  543
     |||||||||||||||||||||||||||||||||||||||||
 169 ysLeuHisSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAla  185

 544 TGCCGCCGGAGGGGACCGCCCTCACTGGCCACCTGAGGACCGACCGGTGG  593
     ||||||||||||||||||||||||||||||||||||||||||
 185 CysArgArgArgAspAlaLeuArgSerGlyHisLeuArgThrHisSerIleAs  202

 594 TAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGT  643
     |||||::::||||||||||||||||||||||||   :::||
 202 pLysProTyrLysCysSerPheCysGlyArgSerTyrArgSerGlnCysSerS  219

 644 CTTTAGAGGAACATAAAGAGCCGCTGCCACAACTACTTGGAAAGCATGGGC  693
     |||||||||:::||||||||||   :::||||||||||||||
 219 erLeuGluGluHisLysAspArgCysHisSerTyrLeuGlnGlyMetGly  235

 694 CTT......CCGGGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCA  737
     |||           |||||||           ||||||
 236 LeuCysThrProGluThr..........GluGluIleHisHi  246

 738 CAGTGAAATGCCAGAGACCTGTCAAGATAGGATCAGAGAGATCTCTCG  787
     |  :::::|                  |||||||||||||::::||||
 246 sArgAsnLeuUlysAlaGluMet.........GlySerGluArgAlaLeuV  260

 788 TGCTGGACAGACTAGCAAGTAATGTCGCAAACGTAAGAGCTCTATGCCT  837
     |||||||||||||||||||::||||||||||||||||||||||
 260 alLeuAspArgLeuAlaSerAsnValAlaLysArgLysSerMetPro  276
```

```
1200 CAACAACGAGGAGGAGCAGCCCAGC...................G 1222
     ||||||||||||::: ::
 407 rAsnAsnGluGluArgSerAlaGlyValSerGlyThrAlaAlaThrGlyG  424

1223 GTCTTATCTACCTGACCAACCACATCGCCCGAGCGCGCAACGCGTGTCG 1272
     |||||||||||||||||||||::||||::||
 424 lyLeuIleTyrLeuThrAsnHisMetAlaProGlyMetArgAsnGlyGly  440

1273 CTC..........AAGGAGGAGCACCGCCTACGACCTGCTGCCGCGC 1310
     :::||||||  ::::||  ||||||||
 441 LeuProGlyValLysGluGluGlnIleArgHisPheGluAlaLeuArgAl  457

1311 CGCC..........TCCGAGAACTCGCAGGACGACGCCTCCGCCGTGGTCA 1348
     ||||          |||:::::||:::::::::||||||
 457 aAlaGlyMetAspLeuSerIleAlaSerGlyAlaSerGlyPheLysValLeuS  474

1349 GCACCAGCGGGGAGCCAGATGAAGGTGTACAAGTCGAACACTGCCGGGTG 1398
     || ::|||||||||||||||:::|||:||| ||||||||||||||
 474 erGlyAspGlyGluGluLeuArgAlaTyrArgCysIleHisCysArgVal  490

1399 CTCTTCCTGGATCACGTCAATGTACACCATCCAGTGGGCTGCCAGGCTT 1448
     ||||||||||||||||||||||||||:::||||||||||||||||
 491 LeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisGlyPh  507

1449 CCGTGATCCTTTGAGTGCAACATGTGCGCTACCACAGCCAGGACCCGT 1498
     |||||||||||||||:::||||||||||||||||||||||||
 507 eArgAspProPheGluCysAsnLeuCysGlyTyrArgSerGlnAspArgT  524

1499 ACGAGTTCTGTCGCACATAACGCAGGGGAGCACCGC 1536
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 524 yrGluPheSerHisIleThrArgGlyGluHisArg  536
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OC   Rajiformes; Rajidae; Raja.
OX   NCBI_TaxID=33514;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20318730; PubMed=10861066;
RA   Haire R.N., Miracle A.L., Rast J.P., Litman G.W.;
RT   "Members of the ikaros gene family are present in early representative
RT   vertebrates.";
RL   J. Immunol. 165:306-312(2000).
DR   EMBL; AF163847; AAF87270.1; -.
DR   HSSP; P15822; 1BBO.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 5.
DR   SMART; SM00355; ZnF_C2H2; 6.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   DNA-binding; Metal-binding; Zinc-finger.
SQ   SEQUENCE   522 AA;   59360 MW;   AAF305808E9EA75E CRC64;

alignment_scores:
                Quality: 1396.00   Length: 493
                  Ratio: 3.598   Gaps: 8
     Percent Similarity: 78.702   Percent Identity: 55.984

alignment_block:
US-08-711-417C-165 x Q9I8W2

Align seg 1/1   to: Q9I8W2   from: 1   to: 522

    112 TCCACCACCTCGGGAGGACAGCAGCAAAAGTCCAAGAGTGACAGAGTCGTGGC 161
        ::::::||| :|||||||| |||||| ||| :::
     32 ThrSerThrProAsnGlyGlnTyrSerSerLeuSerHisMetThrAsnLy 48

    162 CAGTAAATGTTAAAGTACAGACTTCAGATGATGAAGAAGAATGGGCGTGCCT 211
        :::::::::|||::|||:::||| :|||||||||:||::||:|:||||
     48 sAsnSerIleLysIleGluMetHisSerAspGluAspGlyLysAlaL 65

    212 GT...GAAATGAATGGGGAAGAATGTCGGAGGATTTACGAATGCTTGAT 258
        :::||:: |||||:|| ::::|||||| :::|||
     65 euLysGlnMetAspLeuAlaArgSerLysGluGluMetSerThrMetAsp 81

    259 GCCTCGGGAGAGAAAATGAATGGCTCCACAGGGACCAAGGCAGCTCGGC 308
        ||| ::: ::|||:|||||| ::|||||||||
     82 GluSerValValGluSerAsnGlyLeuThrGluSerAsnGlnGlyGlnGl 98

    309 TTTGTCGGAGTTGGAGGCATTCGACTTCTAACCGAAAACTAAAGTGTG 358
        :::::::|| ||||||||||||||||||||||||||||||||||
     98 uMetGlnAlaGluGlyGlyIleArgLeuProAsnGlyLysLeuLysCysA 115

    359 ATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCACAAA 408
        ::||||||||||||||||||||||||||||||||||||||||||||
    115 spIleCysGlyMetValCysIleGlyProAsnValLeuMetValHisLys 131

    409 AGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGCCTC 458
        |||||||||||||||||||||||||||||:::|||||||||||||||
    132 ArgSerHisThrGlyGluArgProPheHisCysAsnGlnCysGlyAlaSe 148

    459 ATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGG 508
        |||||||||||||||||:::||||:::::|||||||||::||||||
    148 rPheThrGlnLysGlyAsnLeuLeuArgHisValLysLeuHisThrGlyG 165

    509 AGAGCCCTTCAAATGCCACCTCTGCAACTACGGCCTCCCGCCGGAGGGAC 558
        ||||||||||||||::::|||||||||||||||||||||||||||
    165 luLysProPheLysCysProPheCysSerTyrAlaCysArgArgArgAsp 181

    559 GCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCTCACAAATG 608
        |||||||||||||||||||||||||||||||||||||||||||||||
    182 AlaLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCy 198

    609 TGGATATTGTGGCCGAAGCTATAAACACGGAACGTCTTTAGAGGAACATA 658
        :::::||||||||||||||||||||||||||||||||||||||||
    198 sAsnTyrCysGlyArgSerTyrLysGlnSerGlnSerLeuGluHisL 215

838 CAGAAAATTCTTCTTGGGGACAAG..........GGCCTGTCCGACACGCC 875
    ||||||||::||:::||:::||| ||| :::|||
277 GlnLysPheIleGlyGluLysGlnPheCysLeuGlyTyrGlnAspLeuGl 293

876 CTACGACAGTGCC...ACGTACGAGAAGGAGAACGAAATGATGAAGTCCC 922
    ||| ||||| |||||::::|||||||||||:::|||
293 nTyrThrSerAlaProSerTyrGluLysGluGlyGluMetMetGlnAlaA 310

923 ACGTGATGGACCAAGCCATCAACAACGCCATCAACTACCTGGGGCCCAG 972
    :: |||||||||||||||||:::|||||:|||||||||||||||||
310 rgPheMetAspGlnAlaIleAsnAsnAlaIleSerTyrLeuGlyAlaGlu 326

973 TCCCTGCGCCCGCTGGTGCAGACGCCCCCGGGC...GGTTCCGAGGTCGT 1019
    ||:::: :::|||||||||||||||::   :::|||:::||
327 SerLeuArgProLeuValGlnThrProProAlaProThrAlaGluMetVa 343

1020 CCCGGTCATCAGCCCGATGTACCAGGCGCGTCGGAGGGCCACCC 1069
     | ||||||||||||||||||||||||||:::||||||||||||
343 lSerValIleSerSerLeuTyrProLeuSerLeuThrArgSerAspThr. 359

1070 CGGGCTCCAACCACTCGGCCCCAGGACAGCGCCCCTGGAGTACCTGCTGCTG 1119
     |||||| :: :::|||:::||
360 ....SerAsnGlyHisProArgValValAlaAlaThrGluAsnSerGlySer 374

1120 CTCTCCAAGGCCAAGTTGGTGCCCTCCGGAGCGCGAGGCGTCCCCGAGCAA 1169
     ||||| :::||| ||||||||||||||
375 GlnValLysAlaLysLeu.......GluArgGlyGlySerProSerAs 388

1170 CAGCTGCCCAAGACTCCACGGACCACCGGAGCAACAACGAGGAGCAGCGCA 1219
     |||||||||||||||||||||||||||||||||||||||||||||||
388 nSerCysGlnAspSerThrAspThrGluSerAsnHisGlu.......... 401

1220 GCGGTCTTATCTACCTGCAACACCACCATCGCCCGACGGCGCGCAACGCGTG 1269
     ||| |||| :::|||||::: |||
402 ..GlyGlnAlaTyrLeuGlnHisHisMetMetAlaProArgPheArgAsn 417

1270 TCGCTC........AAGGAGGAGCACGGCGCCTACGACCTGCTGCGCGC 1310
     ::||| |||| ::: :::|||||||||||||||||||
418 GlyLeuAlaLeuAlaLysGluAsnProLysProPheAspIleValLysAl 434

1311 CGCCTCCGAGAACTCGCGAGAGACGGCGCTCCGCGTGTCAGCCACCAGCGGGG 1360
     ||||:: ::::::::|||||||||||||||:::|||||||||||||||
434 aAlaThrGlyProGlyArgGluMetLeuLysValMetThrAsnGluGlyG 451

1361 AGCAGATGAAGGTGTACAAGTGCAAACACTGCGGGTGCTCTTCCTGGAT 1410
     ||||||||||||:::||||||||||||||:::|||||||:::|||||
451 luGlnValArgValTyrLysCysAspHisCysArgValLeuTyrLeuAsp 467

1411 CACGTGCATGTACACCCAACCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTT 1460
     :::||||||||||||||||||||||||||||||||||||||||||||||||||
468 TyrValMetPheThrIleHisMetGlyCysHisGlyPheArgAspProPh 484

1461 TGAGTGCAACATGTGCGGCTACCAGCAGCAGGACCGGTACGAGTTCTCGT 1510
     ||:::||||||||||||||||||||||||||||||||||||||||||||
484 eGluCysAsnValCysGlyTyrArgSerArgAspArgTyrGluPheSerS 501

1511 CGGCACATAACGCGGAGGGAGCACCGCCTTC 1539
     :::||||||||||||||||||||||||::
501 erHisIleAlaArgGlyGluHisGlyTyr 510

seq_name: sp_vertebrate:Q9I8W2

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1514 ACATAACGCGAGGGGAGCACCGCTTCCAC 1542
     ||||::::||||||||||||||||| |||||
 513 isIleValArgGlyGluHisThrPheHis 522

seq_name: sp_vertebrate:Q90XA2

seq_documentation_block:
ID   Q90XA2            PRELIMINARY;      PRT;    434 AA.
AC   Q90XA2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   IKAROS.
OS   Brachydanio rerio (zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Willett C.E., Kawasaki H., Lin S., Amemiya C.T., Steiner L.A.;
RT   "Ikaros expression as a marker for lymphoid progenitors during
RT   zebrafish development.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416371; AAL11907.1; -. 9B74FBF4EB647FC2 CRC64;
SQ   SEQUENCE  434 AA;  47965 MW;  9B74FBF4EB647FC2 CRC64;

alignment_scores:
                   Quality: 1373.50         Length:     530
                   Ratio:    3.643          Gaps:        10
Percent Similarity:  71.132     Percent Identity:  51.698

alignment_block:
US-08-711-417C-165 x Q90XA2

Align seg 1/1  to: Q90XA2   from:  1  to: 434

   1 ATGGATGCTGACGAGGGTCAAGACATGTCTTTCTCATCAGGGAAGGAAGAAG 50
     |||||||||||||||||||||          ::||||||||||||||||||||
   1 MetGluThrGluAlaGlnGluMetSerGlnIleThrGlyArgAspSe 17

  51 CCCG...CCTGTAAGGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGA 97
     ||||           ::::::::        ||||||  |||||||
  17 rProMetAsnAlaAsnGluGlyGlyGlyGlnAspGluAlaMetProV 34

  98 TCCCCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGT 147
     ::||||||||||||||::::::|||  |||||||||||||||||||||
  34 alProGluAspLeuSerAlaSerThrGlyLeuGlnHisAsnAsnArgThr 50

 148 GACAGAGTGCTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGA 197
     ||:||          ::          |||||||||||||||||||
  51 AspLysProLeu.........................Ser 429

 198 GAATGGGCTGCCTGTGAAATGAATGGGGAAGAATGTGCGGAGGATTTAC 247
     ::|||         ::  ||||||||||||||||||||
 430 ProAlaTyrThrLysGluLeuGluAlaThrLysValLe 446

 248 GAATGCTTGATGCCTCGGGAGGAGAAAATGAATGGCTCCCCACAGGACCAA 297
     ::||||||||         ||||||||        |||||||||
 446 uSerHisThrSerLysGluIleTyrArgValPheSerGluGlyGluGlu 463

 298 GGCAGCTCGGCTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGGAAA 347
     ||||||||||||||||||||||||||||||||||||||||||||||
 463 lnIleArgAlaPheLysCysGluHisCysArgValLeuPheLeuAspHis 479

 348 ACTAAAGTGTGATATCTGTGGATCATTTGCATCGGCGCCAATGTGCTCA 397
     ||||||||||::||||||||||||||||||||||||||||||||||||||
 480 ValMetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGl 496

 398 TGGTTCACAAAGAGAAGCCACACTGGAGACACGGCCCTTCCAGTGCAATCAG 447
     ||||||||||||||||||||||||||||||||||||||||||||
 496 uCysAsnIleCysGlyTyrArgSerHisAspArgTyrGluPheSerArgH 513
```

```
 659 AAGAGGCCTGCCACAACTACTTGGAAAGCATGGCCTTCCGGGCACACTG 708
     ||||||||||::||||||||||||||||    |||:::::||  :::::::
 215 ysGluArgCysHisAsnTyrLeuGluSerMetAlaAlaAlaGln 231

 709 TACCCAGTCATTAAAGAAGAAACTAAG...CACAGTGAAATGGCAGAAGA 755
     :::::||||||||||||:||||||||     ||||||||:||  |||:||
 232 ProMetAsnHisGlnAspTyrLysAspHisAsnThrAlaAlaAspGl 248

 756 CCTGTGCAAGATAGGATCAGAGAGATCTCGTGCTTGGACAGACTAGCAA 805
     |||||||     ||||||    ||||||||||||||||||||||||||||
 248 nIleProLeuMetGlnPheGlnArgProAlaValIleGluArgLeuAlaS 265

 806 GTAATGTCCCAAAACTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGAC 855
     |||||::::|||||||||||||||||||  ||||||:::||:::
 265 erAsnMetGlyLysArgLysSerSerThrProGlnLysPheValGlyGlu 281

 856 AAGGGCCTGTCCGACACGCCCTACGAC...............AGTGCCAC 890
     |||             :::  :::    |||                ||
 282 LysPheMetArgLeuAsnTyrProAspIleAsnCysAsnMetAsnLeuAs 298

 891 GTACGAGAGGAGAACGAAATGATGAAGTCCCACGTGATGACCAAGCCA 940
     :|||||||||||  |||:::|||  ||||:|:||||||||||||||||||
 298 nTyrGluLysGluAlaGluPheMetHisSerHisAsnMetAspGlnAlaI 315

 941 TCAACAACGCCATCAACTACCTGGGGCCAGTCCTGCCCGCTGGTG 990
     |||||||||||||||||||||||||||||||||||||||||||
 315 leAsnAsnAlaIleThrTyrLeuGlyAlaGlyLeuSerLeuArgProLeuMet 331

 991 CAGAGCGCCCCCGGGCGGT...TCCGAGGTGGTCCCGGTCATCAGCCCGAT 1037
     |||         ||||||    :::||||:::|||||||||:|||||
 332 GlnHisGlnProSerSerMetAlaGlyGluValValProValMetAsnSerVa 348

1038 GTAC...CAGCTGCAC........AGGCCCTCGGAGGGCACCCCGCGCT 1075
     ||||    ||||||:         ||:      ::  ::  |||||
 348 lTyrSerGlnIleTyrHisProThrArgLeuGluArgProSerSerArg 365

1076 CCAACCACTCGGCCCCAGGACACGCCCGGCGGTGAGTACCTGCTGCTCTCC 1125
     ::               ::||||||||    :::     |||
 365 luIleThrGluSerHisGluAsnThrValAspGlyProIleSerLeuIle 381

1126 AAGGCCAAGTTGGTGCCTCCGAGCGCCGAGGCGTCCCGAGCAACAGCTG 1175
     ::||||||                |||||||||||||||||||||||||
 382 ArgAlaLysAsnProThrThrGluArgValMetSerProSerHisSerCy 398

1176 CCAAGACTCCACGGACACCGGAGCAACAACGAG.........GAGC 1213
     |  |||||||||||||||||||||||||||||          :::|
 398 sLeuAspSerThrAspThrGluSerSerHisAspAspArgSerAlaGlnG 415

1214 AGCCCAGCGGTCTTATCTACCTGACCAACCACCACCGCCCGACGCGCCGAA 1263
     |||  :::  |||||         ||  ||||||||||||||||||||||
 415 lnHisProGlyValProAlaLeuThrProGlnSerLysArg......Ser 429

1264 CGCGTGCCTGCTCAAGGAGGAGCACCGGCGCTACGACCTGCTGCGGCCGGC 1313
     :::            |||||  ::  :::||||||||||||||||||||
 430 ProAlaTyrThrLysGluLeuThrLysAlaLeuGluAlaThrLysValLe 446

1314 CTCCGAGAACTCGCCAGGACGCGCTCCGCGTGGTCAGCACCAGCGGGGAGC 1363
     :::||||||:::||||    ||||||   ::|||||||
 446 uSerHisThrSerLysGluIleTyrArgValPheSerGluGlyGluGlu 463

1364 AGATGAAGGTGTACAAGTGCGAACACTGCCGGGGTGCTCTTCCTGGATCAC 1413
     ||:||||||||||||||||||||||||||||||||||||||||
 463 lnIleArgAlaPheLysCysGluHisCysArgValLeuPheLeuAspHis 479

1414 GTCATGTACACCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTTTGA 1463
     ||||||||||||||||::|||||||||||||||||||||||||||||||
 480 ValMetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGl 496

1464 GTGCAACATGTGCGGCTACCAGCAGCCAGGACCCGTACGAGTTCTCGTCGC 1513
     |||||||||:::|||||||||||||||||||||||||||||||||||
 496 uCysAsnIleCysGlyTyrArgSerHisAspArgTyrGluPheSerSerH 513
```

```
  55 .................GlyGluArgProPheGlnCysAsnGln 63

 448 TCCGGGGCCTCATTCACCCAGAAGGCAACCTGCTCCGGCACATCAAGCT 497
     ||||||||||||||||||||||||||||||||||||||||||||
  64 CysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLe 80

 498 GCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCGCAACTACGCCGCTGCC 547
     ||||||||||||||||||||||||||||||||:||||||||||||
  80 uHisSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCyssA 97

 548 GCCGGAGGACGGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAA 597
     |||||||||||||||||||||||||||||||||||||||||||
  97 rgArgArgAspAlaLeuThrGlyHisHisArgThrHisSerValGlyLys 113

 598 CCTACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTT 647
     |||||:::::||:||||||||||||||::||||||||:::|||||
 114 ProHisLysCysAlaTyrCysGlyLysArgTyrLysGlyGlnArgSerLe 130

 648 AGAGGAACATAAAGACGCGTCCACAACTACTTGGAAAGCATGGGCCTTC 697
     ||||||||||||||:::::||||||||||||||||::|||||||||
 130 uGluGluHisLysLysGluArgCysHisAlaAsnTyrLeuGlnCysMetGlyLeuG 147

 698 CGGGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATG 747
     :::::||||||| ::::::|||||||||||||:::::::|||
 147 lnAsnSerIleTyr...ThrValLysGluGluAsnSerGlnAsnGluGln 162

 748 GCAGAAGACCTGTCAAGATAGGATCAGAGAGATCTCTGCTGCTGGACAG 797
     ||||||                :|:::||||:|::||||||||||
 163 ArgGluAspMet.......ProAlaSerGluArgAlaLeuValLeuAspAr 177

 798 ACTAGCAAGTAATGTCGCCAAACGTAATGCCTAAGAGTCTATGCCTCAGAAATTTC 847
     |::::||:::||||||||||||||||||||||||::||||||
 177 gIleAlaAsnAsnValAlaLysArgGlySerSerMetProGlnArgPheV 194

 848 TTGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAG 897
     ::||:::::::  ::::::||:::::||||||||
 194 aIleGluAsnArgLeuSerGluSerPheGluSerGlySer...... 208

 898 AAGGAGAACGAAATGATGAAGTCCCACGTGATGACCAAGCCATCAACAA 947
     :::|||::||::|||||:||||||||||||||||||||::||
 209 ......GlyGluLeuMetGlnProHisValIleAspGlnAlaIleAlaAsnSe 223

 948 CGCCATCAACTACCTGGGGCCGAGTCCCTGGCCCCGGTGGTGCGAGACGC 997
     ::||||||||||||||||||||||||||||||||||||||
 223 rAlaIleSerTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrS 240

 998 CCCCGGCGGTTCCGAGGTGTGTCCCGGTCATCAGCCCGATGTACCAGCTG 1047
     ::|||||||||||      |||:||||||||||||||:::|||
 240 erProGlySerAlaAspMet.....ValValSerProLeuTyrAsnLeu 254

1048 CACAGGCGCGTCCGGAGGCCACCCGGCCACCCAACCACTCGGCCCAGGACAG 1097
     |||  :::||||::  ||    :::|||||||||||:::|||||
 255 His...LysSerGlnThrAlaGluGluArgAlaGlyAlaAsnGlyValSerAlaLysAspSe 270

1098 CGCCGTGGAGTACCTGCTCTGCTCTCCAGGCCAAGTTGGTGCCCTCGG 1147
     |||:|||||||||::::||||||||||||||::  ||||||||
 270 rAlaAlaGluHisLeuLeuCysSerLeuSerSerLysSerSerAlaSerValA 287

1148 AGCGGCGAGGCGTCCCGAGCAACAGCTGCCAGACTCCACGGACACCGAG 1197
     :::::|||||||||||||||||||||||||||||||||||||
 287 spLysAspGlySerProSerGlyGlnAsnAspSerThrAspThrGlu 303

1198 AGCAACAACGAGGAGCAGCGCAGC................. 1221
     |||||||||||||||::  :::
 304 SerAsnAsnGluGluGlnArgSerAlaGlyValAlaGlyThrAlaAlaThrGl 320

1222 .GGTCTTATCTACCTGACCAACCACCATCGCCCCGACGCGCGCACGCGCGTGT 1270
     |||||||||||||||||||  :::::  ::::::|||
 320 yGlyLeuIleTyrLeuThrAsnHisMetAlaProGlyMetArgAsnGlyGlyG 337

1271 CGGTC.......AAGGAGGAGCACCGCCTACGACCTGCTGCGCC 1308
     ::|||                   ::::::  |||||
 337 lyLeuProGlyValLysGluGluGlnArgHisPheGluAlaLeuArg 353
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1309 GCCGCC...........TCCGAGAACTCGCCGGCACATCAAGCT 1346
     |||||                |||    :::::::::::::::||:
 354 AlaAlaGlyMetAspLeuSerIleAlaSerGluGlyPheLysLysLe 370

1347 CAGCACCACGCCGGGGAGCCAGATGAAGGTGTACAAGTGCGAACACTGCCGGG 1396
     :||    ::||||||||||||||||||||||||:::||  |||||||||
 370 uSerGlyAspGlyGluGluLeuArgAlaTyrArgCysIleHisCysArgv 387

1397 TGCTCTTCCTGGATCACGTCATGTACACCATCCACATGGGCTGCCACGGC 1446
     |||||||||||||||||||||||||||||||||||||||||||||||
 387 aLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisGly 403

1447 TTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCAGCCAGGACCG 1496
     |||||||||||:::||||||||||||||:::||||||||||||||||
 404 PheArgAspProPheGluCysAsnLeuCysGlyTyrArgSerGlnAsnApr 420

1497 GTACGAGTTCTGTCGCCACATAACGCGAGGGAGCACCGC 1536
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 420 gTyrGluPheSerHisIleThrArgGlyGluHisArg 433
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seq_name: sp_vertebrate:Q90WJ6

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alignment_scores:
        Quality: 1351.50           Length:     522
          Ratio:    3.643          Gaps:         9
Percent Similarity: 71.073    Percent Identity: 51.724

alignment_block:
US-08-711-417C-165 x Q90WJ6

Align seg 1/1  to: Q90WJ6  from: 1  to: 428

  1 ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGGAAGGAAAG 50
    ||||:|  :::||||:|||||||||||||:|||||:||:::::::||
  1 MetGluMetGluGluAlaGlnGluMetAlaAlaGlnMetProGlyArgAspSe 17

 51 CCCCCCTGTAAGCAGCATACTCCAGATGAGGGCGGCCATGCCGATCC 100
    ||||||::::||||||||||  :::::|||||||||||||||||||
 17 rProProAlaAsnGluAlaSerGluGluAlaGluGluProMetAlaValP 34

101 CCGAGGACCTCTCCACCACCTCGGGAGCAGCAGCAAAGTCCAAGAGTGAC 150
    |||||||||  :::||||||||||||  ||||||||||||||||||
 34 roGluAspLeuSerAlaGlySerAlaHisGlnGlnAsnAsnArgGlyAsp 50

151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
    :::
 51 Lys................................................ 51
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us-08-711-417c-165.rspt

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                |||||||::||             ||||||||||||||||::::::|||              :::       |
272 pSerAlaAlaGluAsnLeuLeuLeuLeuSerAsnSerLysSerAlaSerS  289

1145 CGGAGGCCGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACC  1194
     ||||::::::|||:::|||||||:::||   ||||||||||||||||||
289 erGluLysAspGlySerProSerHisSerGlyGlnAspSerThrAspThr  305

1195 GAGAGCAACAACGAGGAGCAGCAGCCGGT...........CTTATCTA  1232
     ||||||||::  :::::::|||||||::::   ::|||          ||||||
306 GluSerAsnAsnGluAspArgThrGlyGlyProProSerLeuIleTy  322

1233 CCTGACCAACCACATC...........GCCCGACGGCGGCCAACGCGTGTCGC  1273
     |||||||::::||||                :::|||:::|||           :
322 rLeuThrSerHisIleAsnProGlyValArgAsnGlyValLeuProLeuV  339

1274 TCAAGGAGGAG...CACCGGCCTACGACCTGCTGCGCGCCTCCGAG  1320
     ::||||||||       ::|||   |||::   ::|||:::||||||||||
339 alLysGluGluGlnLnArgGlnTyrGluAlaIleArgValSerMetGlu  355

1321 AACTCGCAGGACGCGTCCGGTGGTCAGCACCAGCCGGGAGCAGATGAA  1370
     ::::::::::::||||||||||::||||||||||||||::::::|||||||||
356 MetAlaSerGluGlyPheLysValThrAlaAspGlyGluGlnValTh  372

1371 GGTGTACAAGTGCGAACACTGCGGGTCCTCTTTCCTGATCACGTCATGT  1420
     ::||:::|||||||||||||||||||||||||||||||||||||
372 rAlaTyrArgCysGluHisCysGlyValLeuPheLeuAspLeuValMetT  389

1421 ACACCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAAC  1470
     |||||||||||||||||||||||||||||||::|||
389 yrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluCysAsn  405

1471 ATGTGCGGCTACCACAGCCAGGACGCCGGTACGAGTTCTCGCCACATAAC  1520
     ::||||||::|||||||||||||||||||||||||||||||||||
406 LeuCysGlyHisArgSerGlnAspArgTyrGluPheSerSerHisIleTh  422

1521 GCGAGGGGAGCACCGC  1536
     ||||||   ||||||
422 rArgGlyValHisArg  427
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seq_name: sp_vertebrate:Q90W82

alignment_scores:
                     Quality: 1341.50   Length: 581
                     Ratio: 3.240   Gaps: 18
Percent Similarity: 71.256   Percent Identity: 49.225

alignment_block:
US-08-711-417C-165 x Q90W82

Align seg 1/1 to: Q90W82   from: 1   to: 563

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201 TGGGCGTGCCTGTGAAATGAATGGGAAGAATGTGCGGAGGATTTACGAA  250

51  ..................................................   51

251 TGCTTGATGCCTCGGAGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC  300

51  ..................................................   51

301 AGCTCGGCTTTGTCGGGAGTTGGAGGCCATTCGACTTCCTAACGGAAAACT  350

51  ..................................................   51

351 AAAGTGTGATATATCTGTGGGATCATTTGCATCGGGCCCAATGTCGCTCATGG  400

51  ..................................................   51

401 TTCACAAAAGAAGCCACCTGAGAACGCCCTTCCAGTGCAATCAGTGC  450
                           ||||||||:::|||:::|||||
52          GlyGluArgProPheHisCysSerGlnCys  61

451 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACATCAAGCTGCA  500
    |||||||||||||||||||:::::|||||||||||||
62  GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi  78

501 TTCCGGGAGAAGCCCTTCAAATGCCACCTCTGCCAACTACGCGTCTTTAGA  550
    |||||||||||||||   |||::|||||||||||||
78  sSerGlyGluLysProPheLysCysHisArgCysSerTyrAlaCysArgA  95

551 GGAGGACGGCCCTCACTGGCCACCTGAGGACGGCCACTCCGTTGGTAAACCT  600
    ||||||||||||||||:::|||||||||||||||||
95  rgArgAspAlaLeuThrGlyHisHisSerValGlyLysPro  111

601 CACAAATGTGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGA  650
    |||||||||||||||   |||:||||||||||||
112 HisLysCysAlaTyrCysGlyArgSerTyrGluGlnAsn...SerLeuAs  127

651 GGAACTAAAGAGCGCTGCCACAACTACTTGAAAGCATGGCCTTCCGG  700
    :|||||||||||||   ||||||||   ::||
127 pGluHisLysGluArgCysHisAsnTyrLeuGlnCysMetGlyPheGlnA  144

701 GCACACTGTACCCAGTCATTAAAGAAGAAGAAACTAAGCACAGTGAAATGGCA  750
    :::::|||||   |||:|||||||||   ||||||||||||||
144 snSerIleTyrThrValValGlyGluSerAsnGlnAsnGluGlnAsnArg  160

751 GAAGACCTGTGCAAGATAGGATCAGAGGAGATCTCTGCTGGACAGACT  800
    ||||||||||   :::  :::||:::|||::|||||||||||||||||
161 GluAspLeuSerGlnThrGlySerAspArgAlaLeuValLeuAspPArgLe  177

801 AGCAAGTAATGTGCCAAACGTAAGACGTCTATGCCTCAGAAATTTCTTG  850
    |||::|||||||||||||||::::||||||||||::::|
177 uAlaAsnAsnValAlaLysArgLysSerThrMetProGlnLysPheValG  194

851 GGGACAAGGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAG  900
    |||||||||||||   |||:::  ||||||||
194 lyAspLysArgGlyLeuSerAspLeuSerTyrAspSerGlyGlyAla...  207

901 GAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACAACGC  950
    :::|||:::::::||   ||||||||||||||||::||
208 ...GlyGluLeuIleGlnProHisValIleAspGlnAlaIleAsnSerAl  223

951 CATCAACTACCTGGGGGCCCGAGTCCCTGCGCCCGCTGCTGCAGACGCCCC  1000
    ||||::||||||||||||||:::||||||||
223 aIleSerTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrSerP  240

1001 CGGGCGGGTTCCGAGGTGTCCCGGTCATCACCCGATGTACCAGCTGCAC  1050
     ||:::|||   |||   :::::  |||||
240 roAlaSerSerThrAspValGly...LeuGlySerMetTyrProHisHis  255

1051 AGG...CGCTCGGAGGGC...ACCCCGCGCCTCCAACCACTCGGCCCAGGA  1094
     :::  :::::::|||  ::  ::  |||||||::::||
256 LysProAlaAsnAspGlyHisValGlyLyrArgProSerLeuSerAlaLysSAs  272

1095 CAGCGGCCGTGGGAGTACCTGCCTGCTGCTCCCAAGGCCAAGTTGGTGCCCT  1144
```

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1     ATGGATGCTGACGAGGTCAAGACATGTCTTCTCATCAGGGAAGGAAAG    50
      |||::||| |||   ::  :::  :::  |||||   :::
1     MetGluAla...GluAlaAlaAspGlyTyrIleThrSerGlyAspAsnGl   16

51    CCCCCCTGTAAGGCATACTCCAGATGGGCGATGAGCCCATGCCGATCC    100
      :::||||:::: ::  |||      |||
16    uLeu.........SerProGluArgGluHisSerSerMetAlaIle.     28

101   CCGGAGGACCTC..TCCACCACCTCGGGAGGACAGCAAAGCTCCAAGAGT   147
      ||||||  |||   ||||||||| |||    |||
29    ....AspLeuThrSerSerThrProAsnGlyGlnHisThrSerProSer    43

148   GACAGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGA   197
      ::  :::|||||||||||| ||||||||||||
44    HisValAlaSerThrAsnSerValGluMetGlnSerAspGluGl         60

198   GAATGGGCGCTGCCTGTGAAATGAATGGGGAAGAAATGTGCGAGGAT...T   244
      |::: |||  |||||        :
60    uSerAspArgLys...........ThrPheCysGlnGluAspGluV       72

245   TACGAATGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCACAGGGAC   294
      ::||||::||||| ::||||| :::
72    alArgValLeuAsp..GluGlySerSerLeuGluProLeuThrGlu       87

295   CAAGGCAGCTCGGCT................TTGTCGGGAGTTGG         323
      :::::::||| |||              ||||||||||||| ||
88    AsnAsnGluMetAlaAspAsnArgLysIleGlnGluLeuSerGluGl     104

324   AGGCATTCGACTTCCTAACGGAAAACTAAAGTGTGATATCTGTGGGATCA   373
      |||||||||||||||||||::||||||||||::||||||||:::::
104   yGlyIleArgLeuProAsnGlyLysLeuLysCysAspValCysGlyMetV   121

374   TTTGCATCGGGCCCAATGTGCTCATGTTCACAAAAGAAGCCACACTGGA    423
      :||||||||||||||||||||||||:||||||||||||||||||||
121   alCysIleGlyProAsnValLeuMetValHisLysArgSerHisThrGly  137

424   GAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGG   473
      |||||||||||||||||||||||||||||||||||||||||||||
138   GluArgProPheHisCysAsnGlnCysGlyAlaSerPheThrGlnLysGl   154

474   CAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAAGAGCCCTTCAAAT   523
      ||||||||||||||||||||||||||||:||||||||||||||
154   yAsnLeuLeuArgHisIleLysLeuHisSerGlyGluGluProPheLysC   171

524   GCCACCTTCTGCAACTACGCCTGCCGCCGGAGGACGCCCTCACTGGCCAC   573
      ||  :::||||||||||||||||||||||||::|||
171   ysProPheCysSerTyrAlaCysArgArgArgAspAlaLeuThrGlyHis   187

574   CTGAGGACGACCACTCCGTT.........................       591
      ||||||||||||||||
188   LeuArgThrHisSerValProGlyIleGluMetAlaLeuLeuGlnGluGluIl  204

591   .............................                       591
204   eProValGlnArgLysProLeuAsnTyrSerSerGluLeuLeuTyrMetS   221

592   ..................GGTAAACCTACACAAATGTGGATAT          615
      |||||||||||||||||::|||
221   erGlnAspLeuProSerThrMetGlyLysProHisLysCysAsnTyr      237

616   TGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAAAGAGCG   665
      ||||||||||||||||||||||||||||||||||||||||||
238   CysGlyArgSerTyrLysGlnArgSerSerLeuGluHisLysGluAr      254

666   CTGCCACAACTACTTGGAAAGCATGGGCCTTCCCGGCACA.........   705
      ||||||||||||::::::::|||:::|| :::::
254   gCysHisAsnTyrMetGlnAsnValGlyMetGluAlaGlyLeuProMet.   271

706   ..........CTGTACCCCAGTCATTAAAGAAGAAACTAAGCACAGTGAA   744
      ::  |||   ||:  ||::::|||
271   euSerHisHisValProMet......GluAspCysLysGluGlnGlu      285
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745   ......ATGGCAGAAGACCTGTGCAAGATAGAGATCAGAGATCTCTGT    788
      :::::::: :::  |||||  ||
286   ProValMetAspAsnAsnIleProMetValProPheGluArgProAlaVa  302

789   GCTGGACAGACTAGCAAGTAATGTCCCAAACGTAAGAGCTCTATGCCTC    838
      |:::||||||||||||||::|||||||||||||||||
302   lIleGluLysLeuThrSerAsnLeuGlyLysArgLysSerSerThrProG  319

839   AGAAATTCTTGGGACAAG..............GGCCTGTCCGACACGCCC   876
      |||:|||| |||          |||
319   lnLysPheValGlyGluLysLeuMetArgLeuGlyTyrProAspIleHis  335

877   TACGAC...AGTGCCACGTACGAGAAGGAGAACGAAATGATGAAGTCCCA   923
      ::|||   ::: :||||||||||||||||||::||||||:::|||:
336   PheAspMetAsnLeuSerTyrGluLysGluLeuGluLeuIleGlnSerGl  352

924   CGTGATGGACCAAGCCATCAACAACGCCATCAACTAACTCGGGGCCGAGT   973
      ||||||||||||||||||||||||||||  :::||||||||||::||:
352   nMetMetAspGlnAlaIleHisAsnAlaIleAlaTyrLeuGlyLeuAasps  369

974   CCCTGCGCCCGCTGGTGCAG....ACGCCCCCGGCGGTTCCGAGGTGTC    1020
      |||||:::||||||| ||||    :::::|||||||||||||:::|||
369   erLeuHisProLeuMetGlnHisThrProSerThrIleAlaGluValAla  385

1021  CCGGTCATCAGC..............CCGATGTACCAGCTGCACAGGCGCTC  1058
      |||||| |||              ||||||||||| ::||||
386   ProValSerSerProTyrAlaGlnValTyrHisProAsnArgIleGl     402

1059  GGAGGGCACCCCGCGCTCCAACCACTCGGCCCAGGACGAGCGCCCGTGGAGT  1108
      :::  :||||||||:|||||||||||||||||||||||| ::::|||
402   uArgProIleSerArgGluThrAlaAspSerHisGluAsnAsnMetAspG   419

1109  ACCTGCTGTCGCTCTCCAAGGCCAAGTTGGTGCCCCTGGAGCGGAGGCG    1158
      :::  ||| :|| |||  ||||||||||||||| ::||||||
419   lyProIleSerLeuIleArgProLysSerArgThrGlnAspArgGluGly  435

1159  TCCCCGAGCAACAGCTGCCAAGACTCCACGGACCACCGAGAGCAACAACGA   1208
      |||||:||||||| ||||||||||||||||||||:::::||||
436   SerProSerAsnSerCysLeuAspSerThrAspSerGluSerSerHisGl   452

1209  GGAGCAGCGCAGCGGTCTTATCTACCTGACCAAC.........CACATCG   1249
      |:::::::||| |||   |||                     :: ||||
452   uAspArgGlnSer.......TyrGlnGlyAsnSerAlaLeuAsnProL    466

1250  CCCGACGCGCGAACGGTGTCGCTCAAGGAGGAGCACCCGCCTACGAC      1299
      |||:: ::: ::|||||||||||||||||||||:::|||  ::
466   ysArgLysProSerProAlaTyrMetLysGluAspAlaLeuAsnAsp     482

1300  CTGCTGCGCGCGCCCTCCGAGAACTCGCAGGACGCGCTCCGCGTGGTCAG   1349
      ::: ||||||||||| ::: :|||
483   AlaThrLysAlaSerLysSerGlySerLeuLysAspIleTyrLysValIleLeuAs  499

1350  CACCAGCGGGGACGGGAGCAGATGAAGGTGTACAAGTGGCAACACTGCCGGGTGC  1399
      ::::||||||:|||:::::::::||||||||||||||||
499   nGlyGluGlyGluGlnIleLeuArgAlaPheLysCysGluHisCysSerArgVaL   516

1400  TCTTCCTGGATCACGTCATGTACACCATCCACATGGGCTGCCACGGCTTC   1449
      ||||||||||||||||||||||:::|||
516   euPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisGlyTyr  532

1450  CGTGATCCTTTGACTGCAACATGTGCGCTACCACAGACCGGTA          1499
      ||||||||||||::|||||||||||||||||||||||||
533   ArgAspProLeuGluCysAsnIleCysGlyTyrArgSerGlnAspArgTy  549

1500  CGAGTTCTCTCGCACATAACGCGAGGGGAGCACCGCTTCCAC          1542
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549   rGluPheSerSerHisIleValArgGlyGluHisThrPheHis         563
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seq_documentation_block:
ID   Q9UKT9   PRELIMINARY;   PRT;   509 AA.
AC   Q9UKT9;

Wed Aug 28 10:05:27 2002

us-08-711-417c-165.rspt

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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ZINC FINGER DNA BINDING PROTEIN AIOLOS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPHOMA;
RX   MEDLINE=20021771; PubMed=10552935;
RA   Hosokawa Y., Maeda Y., Takahashi E.i., Suzuki M., Seto M.;
RT   "Human aiolos, an ikaros-related zinc finger DNA binding protein: cDNA
RT   cloning, tissue expression pattern, and chromosomal mapping.";
RL   Genomics 61:326-329(1999).
DR   EMBL; AF129512; AAF13493.1; -.
DR   InterPro; IPR000822; znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 5.
DR   SMART; SM00355; ZnF_C2H2; 6.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   DNA-binding; Zinc-finger.
SQ   SEQUENCE   509 AA;  57943 MW;  28296F1AE2F82450 CRC64;
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US-08-711-417C-165 x Q9UKT9   ..

Align seg 1/1  to: Q9UKT9  from: 1  to: 509
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   22 GACATGTCTTTCTCATCAGGGAAGGAAAGCGCCCCTGTAAGGCGATACTCC 71
      ::  ||| ||:::::::::::: ||| ||||
   28 AspTyrSerLeuThrLysSerHisGluAsnVal.......... 40

   72 AGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACCACCT 121
      ||:::||::: |||  ||||||||:::
   41 .AspSerGlyGluGlyProAlaAsnGluAspGluAspIle.......... 53

  122 CGGGAGCAGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAATGTT 171
      ||:::||::||      |||
   54 ....GlyAspAspSerMetLys...................Val 60

  172 AAAGTAGAGACTCAGAGTGATGAAGAAGAATGGGCGTGCCGTGAAAATGAA 221
      |||  ||  :::||||::  :::|||||:
   61 LysAspGluTyrSerGlyLysArgAspGluAsnValLeuLysSerGluProMe 77

  222 TGGGGAAGAATGTGCGAGGATTTACGAAGCTTGATGCCTCGGGAGAGA 271
      ||::::      |||   ::  ||||||:
   77 tGlyAsn......AlaGluGluProGluIleProTyrSerArgG 92

  272 AAATGAATGGCTCCACAGGGACCAAGGCAGCCAGCTCGGCTTTGTCGGGAGTT 321
      :::       ::  ::  |||||||||||||||||
   92 luTyrAsnGluTyrGluAsnIleLysLeuGluArgHisValValSerPhe 108

  322 GGAGGCATTCGACTTCCTAACGGAAAACTAAAGTGTGATATCTGTGGGAT 371
      :::   :::::::::|||||||||::
  109 AspSerSerArgProThrSerGlyLysMetAsnCysAspValCysGlyLe 125

  372 CATTTGCATCGGGCCCAATGTCATGGTTCACAAAAGAGAGCCACACTG 421
      ||||||:: |||||||||||||||||||||||||
  125 uSerCysIleSerPheAsnValLeuMetValHisLysArgSerHisThrG 142

  422 GAGAACGAGGGCCTTCCAGTGCAAATCAGTGCGGGCCTCATTCACCAGAAG 471
      |||||||||||||||||||||||||||||||||
  142 lyGluArgProPheGlnCysAsnGlnCysGlyTyrAlaSerPheThrGlnLys 158

  472 GGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGAGAAGAGCCCTTCAA 521
      :::|||||| ||||||||||||||||::::||||||||
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  159 GlyAsnLeuLeuArgHisIleLysLeuHisThrGlyGluProPheLy 175
      ||||||||||||||||||||::::||||||||||||
  522 ATGCCACCTCGCAACTACGCCTGCCGCGAGGAGGACGCCCTCACTGGCC 571
      ||||||||||||||::::||||||||||||::::||||||||||
  175 sCysHisLeuCysAsnTyrAlaCysHisArgArgAspAlaLeuThrGlyH 192

  572 ACCTGAGGACGCCACTCCGTTGGTAAACCTCACAAATGTGATAATTGTGGC 621
      ||||||||||||::::|||||| |||||::  |||||||||
  192 isLeuArgThrHisSerValGlyLysProTyrLysCysHisPheCysGly 208

  622 CGAAGCTATAAACAGCGAACGTCTTTAGAGAACCATAAAGAGCGCTGCCA 671
      ||||||||:::      ::  :::::::||||||||
  209 ArgSerTyrLysGlnArgSerLeuGluGluHisLysGluArgCysAsr 225

  672 CAACTACTTGGAAAGCATGGGCCTTCCGGCACACTGTACCCAGTCATTA 721
      :::::::||:::|||  ||||||
  225 gThrPheLeuGlnSerThrAsp...ProGly.............. 234

  722 AAGAAGAAACTAAGCACAGTGAAATGGCGAGAGACCTGTGCAAGATAGGA 771
      ||||||||||||||||||||||||||||||:::  ::::::||||
  235 .....AspThrAlaSerAlaGluAlaArgHisIleLysAlaGluMetGly 249

  772 TCAGAGAGATCTCCGTGCTGGACGACTAGCAGTCAAGTAATGTCGCCAAACG 821
      |||||:::|||||||||||||||||||||||||||||||||||||||
  250 SerGluArgAlaLeuGluValLeuAspArgLeuAlaSerAsnValAlaLysAr 266

  822 TAAGAGCTCTATGCCTCAGAAAATTCTTGGGACAAG...GGCCTGTCCG 868
      ||||||||||||||||||||||||||::::|||::  |||
  266 gLysSerSerMetProGlnLysPheIleGlyGlyLysArgHisCysPheA 283

  869 ACACGGCCTACGACAGTGCC...ACGTACGAAGGAGCAACGAAAATGATG 915
      |||  |||::||| ||||||::   ::||||||||::::||||||||:::
  283 spValAsnTyrAsnSerSerTyrMetTyrGluLysGluSerGluLeuLe 299

  916 AAGTCCCACGTGATGACCAGCCATCAACAACGCCATCAACTACCTCTGGG 965
      ::::::::::||||||||||||||||||:::||||||||||||||||||
  300 GlnThrArgMetMetAspGlnAlaIleAsnAsnAlaIleSerTyrLeuGl 316

  966 GGCCGAGTCCCTGCGCCCGTGGTGCAGACGCCCCCGGGC...GGTTCCG 1012
      |||||||  ::::::::|| ::::||:: ||||||| |||    ||||||
  316 yAlaGluAlaLeuCysProLeuValGlnThrProProAlaProThrSerG 333

 1013 AGGTGGTCCCGGTCATCAGCCGATGTACCAGCTCAC...AGGGGCTCG 1059
      ||||::::||||  ||| ::: |||||::     |||   ||||||||
  333 luMetValProValIleSerSerMetTyrProIleAlaLeuThrArgAla 349

 1060 GAGGGCACCCCCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGTA 1109
      ||||||| ::: :::  ||:: |:::||||||||||||||:::||||
  350 Glu........MetSerAsnGlyAlaProGlnGluLeuGluArgLysse 363

 1110 CCTGCTGCTGTCTCCAAGGCCAAGTTGGTCGTCCCTCGGAGCGGAGGCGT 1159
      ::::::::   ||||||::::||||||||||:: |||||||||||||||
  363 rIleLeuLeuProGluLysSer......ValProSerGluArgGlyLeuS 378

 1160 CCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGCAACAACGAG 1209
      |||||::::::::||||||||||||||||||::::|||||||||:::||
  378 erProAsnAsnSerGlyHisAspSerThrAspThrAspSerAsnHisGlu 394

 1210 GAGCAGCCCAGCGGGTCCTTATCTACCGACCAACCACCATCGGCCGACGCGC 1259
      ||||||||::::|||  ::: :::|||||||||||::::||||||::
  395 Glu...ArgGlnAsnHisIleTyrGlnGlnAsnHisMetValLeuSerAr 410

 1260 GCAACGGCTGTCG.........CTCAAGGAGGAGCACCGCGGCTACGACC 1300
      |||||||||||||          ||||:: ||:::::||||||:::||
  410 gAlaArgAsnGlyMetProLeuLeuLysGluValProArgSerTyrGluL 427

 1301 TGCTGCGCCGCCCTCCGAGAACTCGCAGGACGCGGCTTCCGCGTGGTCAGC 1350
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  427 euLeuLysProProProIleCysProArgAspSerValLysValIleAsp 443

 1351 ACCAGCGGGAGCAGATGAAGGTGTACAAGTGGCGAAACTGCGGGTGCT 1400
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444 LysGluGlyGlyGluValMetAspValTyrArgCysAspHisCysArgValLe 460

1401 CTTCCTGGATCACGTCATGTCATCCACCATCCACATGGGCTGCCACGGCCTTCC 1450
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460 uPheLeuAspTyrValMetPheThrIleHisMetGlyCysHisGlyPheA 477

1451 GTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGACCGGTAC 1500
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477 rgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAspArgTyr 493

1501 GAGTTCTCGCCGCACATAACGGCGAGGGGACCACGGC 1536
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494 GluPheSerSerHisIleAlaArgGlyGluHisArg 505

seq_name: sp_rodent:O08900

seq_documentation_block:
ID  O08900      PRELIMINARY;      PRT;      507 AA.
AC  O08900;
DT  01-JUL-1997 (TrEMBLrel. 04, Created)
DT  01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  AIOLOS (FRAGMENT).
GN  ZNFN1A3.
OS  Mus musculus (Mouse)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Morgan B., Sun L., Avitahl N., Andrikopoulos K., Ikeda T.,
RA  Gonzales E., Wu P., Neben S., Georgopoulos K.;
RT  "Aiolos, a lymphoid restricted transcription factor that interacts
RT  with Ikaros to regulate lymphocyte differentiation.";
RL  EMBO J. 17:2004-2013(1997).
DR  EMBL; AF001293; AAB58795.1; -.
DR  MGD; MGI:1342542; Znfn1a3.
DR  InterPro; IPR000822; Znf-C2H2.
DR  Pfam; PF00096; zf-C2H2; 5.
DR  SMART; SM00355; ZnF_C2H2; 6.
DR  PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_4.
DR  PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
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FT  NON_TER      507      507
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8 ValGluLeuLysSerThrGluGlnProLeuProThrGluSerProAs 24

75 TGAG...GGCGATGAGCCCATGCCGATCCCCGAGGACCTCTCCACCACCT 121
   ::||| :||| |||||||||:|||||:|||||||||||||:|||||||||
24 pAlaLeuAsnAspTyrSerLeuProLysProHisGluIleGluAsnValA 41

122 CGGGAGGACGACGAAAGTCCAAGAGTGACAGAGTCGTGGCCAGTAAT... 168
    ::::: ::: :||||||:|:||||:::|||::::|||||||||||
41 spSerArgGluAlaProAlaAsnGluAspGluAspAlaGlyLeuGlyAspSer 57

169 ......GTTAAAGTAGAGACTCAGAGTGATGAAGAAGAAGAATGGGCGTGCCTG 212
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58 MetLysValLysAspGluTyrSerAspArgAspGluAsnIleMetLysPr 74
```

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213 TGAAATGAATGGAGAAGAATGTGCGGAGGATTACGAATGCTTGATGCCT 262
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74  oGluProMetGly......................AspAlaG 81

263 CGGGAGGAGAAATGAAGTGCTCCACAGCCAGCCAAGGCAGCTCGGCTTTG 312
    :: :::||||||   |||||| :::||||||||||||||||||||||||
81  luGlySerGluMetProTyrSerTyrAlaArgGluTyrSerAspTyrGlu 97

313 TCG............................GGAGTTGGAGGCATTCGACTTCCTAA 341
    |||                            :::  |||   ::
98  SerIleLysGluArgHisValProTyrAspAsnSerArgProThrSe 114

342 CGGAAAACTAAAGTGTGATATCTGTGGGATCATTGCATCGGCCCCAATG 391
    :||||||||:||||||||||||||||||||:::    |||    |||
114 rGlyLysMetAsnCysAspValCysGlyLeuSerCysIleSerPheAsnV 131

392 TGCTCATGGTTCACAAAAGAGCCACTGGAGAACGGCCCCTTCCAGTGC 441
    |||||||||||||||||||||||||||||||||||||||||||||||||
131 alLeuMetValHisLysArgSerHisThrGlyLeuArgProPheGlnCys 147

442 AATCAGTGCGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCACAT 491
    ||||||||||||||||||||||||||||||||||||||||||||||||||
148 AsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIl 164

492 CAAGCTGCATTCCGGGGAGAGCCCTCAAATGCCACCTCTGCAACTACG 541
    ||||||||:::||||||||||||||||||||||||||||||||||||||
164 eLysLeuHisThrGlyGluLysProPheLysCysHisLeuCysAsnTyrA 181

542 CCTGCGCCGGAGGGACGCCCCTCACTGGCCACCTGAGGACGCCACTCCGGT 591
    ||||||||:::||||||||||||||||||||||||||||||||||||||||
181 laCysGlnArgArgAspAlaLeuThrGlyHisLeuArgThrHisSerVal 197

592 GGTAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAAC 641
    ||||:::||||| |||||||||||||||||||||||||||||||||::::
198 GluLysProTyrLysCysGluPheCysGlyArgSerTyrLysGlnArgSe 214

642 GTCTTTAGAGGAACATAAAGAGCCGCTGCCACAACTACTTGGAAAGCATGG 691
    |:||||||||||||||||||||||||::::    ::::||||||||
214 rSerLeuGluHisLysGluArgCysArgAlaPheLeuGlnAsnAsnProA 231

692 GCCTTCCGGGCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGT 741
    |||   :::||||:|||
231 spLeu...GlyAspAlaAlaSerVal..........GluAlaArgHisIle 243

742 GAAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGAATCTCTCGTGCT 791
    :::                ::::::||||||||||::|||||||||||||
244 Lys.................AlaGluMetGlySerGluArgAlaLeuValLe 255

792 GGACAGACTAGCAAGTAAGTGTCGCCAAACGTAAGAGTCTATGCCCTCAGA 841
    ||||||||||||||||||||||||||||||||||||||||||:||||||
255 uAspSerArgLeuAlaSerAsnValAlaLysArgLysSerSerMetProGlnL 272

842 AATTTCTTGGGGACAAG...GGCCTGTTCCGACACGCCCTACGACAGTGCC 888
    |||||:|||:::|||       |||  :||::  ||| ||||:::
272 ysPheIleGlyGluLysArgHisCysPheAspAlaAsnTyrAsnProGly 288

889 ...ACGTACGAGAAGGAGAACGAAAATGATGAAGTCCCACGTGATGGACCA 935
   ::::::::|||||||||||||||||||||||||::||||||
289 TyrMetTyrGluLysGluAsnGluMetGlnThrArgMetMetAspGl 305

936 AGCCATCAACAACGCCATCAACTACCTGGGGCCGAGTCCCTGCGCCCGC 985
    ||||||||||||||||:|||||||||||:||||||||||:||||||||
305 nAlaIleAsnAsnAlaIleSerTyrLeuGlyAlaGluAlaPheArgProL 322

986 TGGTGCAGACGCCCCCGGGC...GGTTCCCAGGTGGTCCCGGTCATCAGC 1032
    ||||||||||||||||||||   |||||||||||||:||||||||||
322 euValGlnThrProProAlaProThrSerGluMetValProValIleSer 338

1033 CCGATGTACCAGCTGCAC...AGGCCGTCGGAG.........GGCACCCG 1070
     ::|||| |||||||||     ::|||||||         |||::||
339 SerValTyrProIleAlaLeuThrArgAlaAspMetProMetGlyAlaPr 355

1071 GCGCTCCAACCACTCGGCCCAGGACAGCGCCGCGTTGGAGTACCTGCTGCTGC 1120
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US-08-711-417C-165 x Q96JP3

Align seg 1/1   to: Q96JP3   from: 1 to: 545

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355 oGlnGlu.....................MetGluLysLysArgIleL 364

                                                                  93
52 CCCCCTGTAAGCGATACTCCAGATGAGGGCGATGAGCCCATG...........
   ||| |||                          ::  ::
14 ProSerCysSerLeuLeuGlnGlySerGlyAspSerLeuGluLysGl 30

1170
1121 TCTCCAAGGCCAAGTTGGTGCCCTCGGAGCGGCGAGGCGTCCCCGAGCAAC
     ||     ||:::||||||||||| ::|||
364 euLeuProGluLysIleLeuProSerGluArgGlyArgGlyLeuSerProAsnAsn 380

                                                                 130
94 .........CCGATCCCGAGGACCTCTCCACCACCTCCGGGAGGAC
         :::||||||||||||  :::   :::
30 uPheLeuGlyAlaProValGlyProSerValSerThrProAsn...SerG 46

1220
1171 AGCTGCCAAGACTCCAGGACACCGAGACAACAACGAGGAGCAGCGCAG
     ||:::||||||||||||||::::::
381 SerAlaGlnAspSerThrArgAspThrArgSerAsnHisGluAspArgGlnHi 397

                                                                 180
131 AGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAG
    |:::||||| ||| |||   :::::|||||:::||||||||
46 lnHisSerProSerArgSerLeuSerAlaAsnSerIleLysValGlu 62

1258
1221 CGGTCTTATCTACCTGACCAACCACATC............GCCCGACGCG
     :::|||::       ||||||:::
397 s......LeuTyrGlnGlnSerHisValLeuProGlnAlaArgAsnG 412

                                                               209
181 ACTCAGAGTGATGAAGAGAATGGG.................CGTGC
    |||||||||||||||:::            |||
63 MetTyrSerAspGluSerSerArgLeuLeuGlyProAspGluArgIle 79

1308
1259 CGCAACGGCGTGTCGCTCAAGGAGCACCGGCGCCTACGACCTGCTCGC
     |||||||||||||:::           |||
412 lyMetProLeu...LeuLysGluValProArgSerPheGluLeuLeuLys 427

                                                            244
210 CTGTGAAATGAATGGGAGAAATGTGCGGAGGAT.................T
    |||  ::   :::  :||||||
79 uLeuGluLysAspAspSerValIleValGluAspSerLeuSerGluProL 96

1358
1309 GCCGCCTCCGAGAACTCCGAGGACGCGGCTCCGCGCTGGTCAGCACCAGCGG
     :::|||::::::||||::::  :||||
428 ProProProIleCysSerLeuArgAspSerIleLeuLysValIleAsnLysGluGl 444

                                                            294
245 TACGAATGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCACAGGGAC
    || :||::|||||| :||||||
96 euGlyTyrCysAspGlySerGlyProGluProHisSerPro......... 109

1408
1359 GGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCACGGCTGCTCTTCCTGG
     ||| |||  :::||||:::||||||||||
444 yGluValMetAspValPheArgCysAspHisCysHisValLeuPheLeuA 461

                                                            344
295 CAAGGCAGCTCGGCTTGTCGGGAGTTGGAGCATTGGACTTCGACTTCCTAACGG
     |||||||||||||||||||
110 .........GlyGlyIleArgLeuProAsnGl 117

1458
1409 ATCACGTCATGTACACCATCCACATGGCTGCCACGGCCGTCCGTGATCCT
     ||:::|||||||||||||||||||||||
461 spTyrValMetPheThrIleHisMetGlyCysHisGlyPheArgAspPro 477

                                                            394
345 AAAACTAAAGTGTGATATCTGTGGGATCATTTGCATCGGGCCCAATGTGC
     |||||||||||||||||||||:::||||||
117 ylysLeuLysCysAspValCysGlyMetValCysIleGlyProAsnValL 134

1508
1459 TTTGAGTGCAACATGTGCGGCTACCACAGCCAGGACCGGTACGAGTTCTC
     ||||||||||||||||||::::||||||||||||
478 PheGluCysAsnMetCysGlyTyrArgSerHisAspArgTyrGluPheSe 494

                                                            444
395 TCATGGTTCACAAAAGAAGAGCCACACTGAGAAGGCAGCCCCTTCCAGTGCAAT
     ||||||||||||||||||||||:::|||||
134 euMetValHisLysArgSerHisThrGlyLysProPheHisCysAsn 150

1536
1509 GTCGCACATACGCGAGGGGAGCACCGC
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494 rSerHisIleAlaArgGlyGluHisArg 503

                                                            494
445 CAGTGCGGGCCTCATTCACCCAGAACGGCAACCTGCTCCGGCACATCAA
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151 GlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLy 167

544
495 GCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTGCAACTACGCCT
     |||||||||||||| :||||||||||||||||
167 sLeuHisSerGlyGluLysProPheLysCysProPheCysAsnTyrAlaC 184

588
545 GCCCGCCGGAGGACGCCCCTCACTGGCCACCTGAGGAGCGACTCC.......
     |||||||||||||||||||||||||
184 ysArgArgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValSer 200

629
589 .........GTTGGTAAACCTCACAAATGTGGATATTGTGGCCGAGCTA
              |||||||||||||||||||
201 SerProThrValGlyLysProTyrLysCysAsnTyrCysGlyArgSerTy 217

679
630 TAAACAGCGAACGTCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACT
     ||||||||||||:::|||||||||||||||||
217 rLysGlnGlnSerThrLeuGluGluHisLysGluArgCysHisAsnTyrL 234

705
680 TGGAAAGCATG.....................GGCCTTCCGGGGCACA
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234 euGlnSerLeuSerThrGluAlaGlnAlaAlaLeuAlaGlyGlnProGly... 249

755
706 CTGTACCCAGTCATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGA
     ||||||||:: |||||||:::    |||
250 .........AspGluIleArgAspLeuArgGluMetValProAs 260

802
756 C...CTGTGCAAGATAGGATTAGGATCAGAGAGATCTTCTCGTCTGCAGACTAG
    |   :::  |||||||| :::||||||||||
260 pSerMetLeuHisSerSerGluArgProThrPheIleAspArgLeuA 277

852
803 CAAGTAATGTCGCCAAACGTAAGAGCTCATGCCTCAGAAATTCTTGGG
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        Ratio: 3.385   Gaps: 17
Percent Similarity: 69.384   Percent Identity: 50.181

alignment_block:

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GN   ZNFN1A4 OR EOS.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=99232954; PubMed=10218586;
RA   Homma Y., Kiyosawa H., Mori T., Oguri A., Nikaido T., Kanazawa K.,
RA   Tojo M., Takeda J., Tanno Y., Yokoya S., Kawabata I., Ikeda H.,
RA   Wanaka A.;
RT   "EOS: a novel member of the Ikaros gene family expressed predominantly
RT   in the developing nervous system.";
RL   FEBS Lett. 447:76-80(1999).
DR   EMBL; AB017615; BAA36213.1; -.
DR   HSSP; P15822; 1BBO.
DR   MGD; MGI:1343139; Znfn1a4.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 6.
DR   SMART; SM00355; ZnF_C2H2; 6.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   DNA-binding; Metal-binding; Zinc-finger.
SQ   SEQUENCE   533 AA;  58167 MW;  7A5FF32C6FFDC372 CRC64;

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alignment_block:
US-08-711-417C-165 x Q9Z2Z2

Align seg 1/1  to: Q9Z2Z2   from:  1  to: 533

 94 CCGATCCCCGAGGACCTCTCCACCACCTCGGGAGGACAGCAAAGCTCCAA 143
    ||||||                   |||:::||:::||||:::|||||||
 22 ProValGlyProSerValSerThrProAsn...SerGlnHisSerSerPr  37

144 GAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATG 193
    |||    :::  ||:::||||||||:::||||:||||:::||||||||||
 37 oSerArgSerLeuSerAlaAsnSerIleLysValGluMetTyrSerAspG  54

194 AAGAGAATGGGCGTGCCGTGAAATGAATGGGAAGAATGTGCGGAGGAT 243
    |||||||||:::||                               |||
 54 luGluSerSerArgLeu........................LeuGlyProAsp  63

244 TTACGAATGCTTGATGCCTCGGGAGAGAAAATG................. 276
    |||:::||||||      :::   :::  |||||
 64 GluArgLeuLeuAspLysAspSerValIleValGluArgSerLeuSe  80

277 .....................AATGGCTCCACAGGACCAAGGCAGCTCGG 307
                         :::|||||  ||| :::  :::|||||||
 80 rGluProLeuGlyTyrCysAspGlySerGlyProGluProHisSerPro.  96

308 CTTTGTCCGGAGTTGGAGGCATTCGACTTCCTAACGGAAAACTAAAGTGT 357
    |||||||::::|||||||||||||||||||||||||||||||||||||
 97 ......GlyGlyIleArgLeuProAsnGlyLysLeuLysCys 108

358 GATATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCACAA 407
    |||:||||||:::||||||||||||||||||||||||||||||||||||
109 AspValCysGlyMetValCysIleGlyProAsnValLeuMetValHisLy 125

408 AAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCT 457
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125 sArgSerHisThrGlyGluArgProPheHisCysAsnGlnCysGlyAlaS 142

458 CATTCACCCAGAAGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGG 507
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277 laAsnSerLeuThrLysArgLysArgSerThrProGlnLysPheValGly 293
    ||:::::::::||||||||    |||    ||||||||||||::||||
853 GACAAG.........GGCCTGTCCGACACGCCCTACGAC......AG 884
    :::|||           ::||||||   ||||||||    ||
294 GluLysGlnMetArgPheSerLeuSerArgAspLeuProTyrAspValAsnSe 310
885 TGCCACGTACGAGAGGAGAGAACGAAATGATGAGCTCCCACGTGATGGACC 934
    |:::  |||||||||:::   ||| :::||   :::||   :::::
310 rGlyGlyTyrGlyLeuLysAspValGluLeuValAlaHisHisSerLeuGluP 327
935 AAGGCCATCAACAACCGCCATCAACTACCTGGGGCCGAGTCCCTGCGCCCG 984
    :::::::::::::   :::||||||||   |||||||||   :::::
327 roGlyPheGlySerSerLeuAlaPheValGlyAlaGlyHisGluHisArgPro 343
985 CTGGTGCAGAGCCCCGGGCGGT......TCCGAGTGGTCCCGTCAT 1028
    |||    :::      |||||||||      :::||||||||||
344 Leu...ArgLeuProProThrAsnCysIleSerGluLeuThrProValIl 359
1029 CAGCCCGATGTAC.........CAGTCGCACAGGCGCTCGGAG.... 1062
     ||||    :::|||         ||| :::||||||||||||
359 eSerSerValTyrThrGlnMetGlnProLeuProGlyArgLeuGluLeuP 376
1063 ..GGCACCCCGCGCTCCAACCACTCGGCCCAGGACAGCGCCGTGGAGTAC 1110
     |||  :::   ||| :::||| |||||||||   ||| :::
376 roGlySerArgGluAlaGlyAlaGlyProGluAspLeuAla...AspGly 391
1111 CTGCTGCTCTCCAAGGCCAAGTTGGTCCCTGAGCGCGAGGCGTC 1160
     ||||||       |||||||||||||||    :::::   ||||
392 GlyProLeuLeuTyrArgProArgGlyProLeuThrAspProGlyAlaSe 408
1161 CCCGAGCAACAGCTGCCAAGACTCCACGGACACCCGAGACAACGAGG 1210
     ||||||||:::||||||||||::::|||||||||||||:::|||
408 rProSerAsnGlyCysGlnAspSerThrAspThrGluSerAsnHisGluA 425
1211 AGCAGGCCAGCGGTCTTATCTACCTG.................... 1236
     :::|||  ||||||||||||||||:::
425 sProArgValAlaGlyValValValSerLeuProGlnIleGlyValProGlnPro 441
1237 ......ACCAACCACATCGCCCGACGCGCGCAACCGTGTCGCTCAAGGA 1280
           ||| :::::|||::::::||
442 ProProThrIleValValGlyArgHisSerProAlaTyrAlaLysGluAs 458
1281 GGAGCACCCGCGCTACGACCTGCTGCGGCGGCCTCCGAGAACTCGCAGG 1330
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458 pProLysProGlnGluGlyLeuLeuArgGlyThrProGlyProSerLysG 475
1331 ACGCGCCTCCGCGTGCTGCAGCACCAGGCGGAGCAGATGAAGGTGTACAAG 1380
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475 luValLeuArgValValGlyLySerGlyGluProValLysAlaPheLys 491
1381 TGCGAACACTGCCGGGGTGCTCTTCCTGGATCACGTCATGTACCACCATCCA 1430
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492 CysGluHisCysArgGlyAlaLeuLeuAspHisValMetPheThrIleHi 508
1431 CATGGGCGTGCCACAGCGTCCCTGATCCTTTGAGTGCAACATGTGCGGCT 1480
     ||||||||||||||||:::   ||||||||||||||||||||||||
508 sMetGlyCysHisGlyPheArgAspProPheGluCysAsnIleCysGlyT 525
1481 ACCACAGGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCGAGGGGAG 1530
     ||||||||||||||||||||||||||:::   :::|||||||||||
525 yrHisSerGlnAspArgTyrGluPheSerSerHisIleValArgGlyGlu 541
1531 CACCGC 1536
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542 HisLys 543
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seq_documentation_block:
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AC   Q9Z2Z2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)

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142  erPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGly   158

508  GAGAAGCCCTCAAATGCCACTCTGCAACTACGCCTGCCACCGCGAGGGA     557
     |||||||||||||||||  ::||||||||||||:  ::|||||||||||
159  GluLysProPheLysCysProPheCysAsnTyrAlaCysArgArgArgAs    175

558  CGCCCTCACTGGCCACCTGAGGACGCACTCC.............GTTG     592
     |||||||||||||||||||||||||||||||             ||||
175  pAlaLeuThrGlyHisLeuArgThrHisSerValSerSerProThrValG    192

593  GTAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACG    642
     ||||||||:::||||||||||||||||||||||||||||||:::::|||
192  lyLysProTyrLysCysAsnTyrCysGlyArgSerTyrLysGlnInSer    208

643  TCTTTAGAGAACATAAAGAGCGCTGCCCAACTACTTGGAAAGCATG..     690
     :::||||||||||||||||||||||||||||||||||||||||:::
209  ThrLeuGluGluHisIleLysGluArgCysHisSerAsnTyrLeuGlnSerLeuSe  225

691  ...............GGCCTTCCGGCACACTGTACCCAGTCA         718
                     ||  |||||||
225  rThrAspAlaGlnAlaLeuThrGlyGlnProGly.............     236

719  TTAAAGAAGAAACTAAGCACAGTGAAATGCCAGAAGAC...CTGTGCAAG  765
     ||||||  :::   |||||   ||||||||
237  .....AspGlulleArgAspLeuGlnMetValProAspSerMetLeuHis  251

766  ATAGGATCAGAGAGATCTCTCGCTGGACAGACTAGCAAGTAATGTCGC    815
     ::::::||||||    ::|||||||||||||||||||||||||||:||
252  ProSerThrGluArgProThrPheIleAspArgLeuAlAsnSerLeuTh   268

816  CAAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGACAAG........  858
     :|||||||||  ||| |||||||||||||::::|||
268  rLysArgLysArgSerThrProGlnLysPheValGlyLysGlnMetA      285

859  .....GGCCTGTCCGACACGCCCTAGGAC.........AGTGCCACGTAC  894
         |||||||||||||||||       ||||  :  |||
285  rgPheSerLeuSerAspLeuProTyrAspValAlaSnAlaSerGlyGlyTyr  301

895  GAGAAGGAGAACGAAAATGATGAGTCCACGTGATGGACCAAGCCATCAA   944
     |||||||  :::::::||||||||   :||||||||  :::::::
302  GluLysAspValGluLeuValAlaAlaHisHisGlyLeuGluProGlyPheGl  318

945  CAACGCCCATCAACTACCTGGGGGCCGAGTCCCTGCCGCCGCTGGTGCAGA  994
     :::::::::  :::||||||||||||||||||||||| |||  :::
318  yGlySerLeuAlaPheValGlyThrGluHisLeuArgProLeu...ArgL  334

995  CGCCCCGGGCGGT.....TCCGAGGTGGTCCGGTCATCAGCCCGATG      1038
     ||||||    |||      ::|||||||:::||||||||||||||||
334  euProProThrAsnCysIleSerGluLeuThrProValIleSerSerVal  350

1039  TAC...........CAGCTGCACAGGGCCTCGGAG......GGCACCCCC  1070
      |||            :::   |||  ||||  |::
351  TyrThrGlnMetGlnProIleProSerArgLeuGluLeuProGlySerAr  367

1071  GCGCTCCAACCACTCGGCCCAGGACAGCAGCCGTGGAGTACCTGCTGC    1120
      ::|||||||||||||||||||||  ::     :::  |||||||
367  gGluAlaGlyGluGlyProGluAspLeuGly...AspGlyGlyProLeuL   383

1121  TCTCCAAGGCCAAGTTGGTGCCCTCGAGGCGCGAGGCCGTCCCCAGCAAC  1170
      ||  :::||||::::           |||||||||||||
383  euTyrArgAlaArgGlySerLeuThrAspProGlyAlaSerProSerAsn  399

1171  AGCTGCCAAGACTCCACGGACAACGAGAGCAACAACGAGGAGCAGCGCAG  1220
      ::||||||||||||||||||||||||||||||||||||||||||||
400  GlyCysGlnAspSerThrAspThrGluSerAsnHisGluAspArgIleGl  416

1221  CGGTCTT......................................A  1228
      |
416  yGlyValGlyIleProSerSerGlySerProProGlnProProProThrI  433

1229  TCTACCTGACCAACCACCATCGCCCGACGCCGCCAACGCCGTGTCGCTCAAG  1278
      ||  :::||||
433  euAspLeuSerAsnProGlnGlyGlnProLysAlaAla.........  13
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433  leValValGlyArgHisSerProAlaTyrAla...............Lys  444

1279  GAGGAGCACCGCCGCTACGAC...CTGCTGCGCGGCCGCCTCCGAGAACTC  1325
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445  GluAspProLysProGlnGlyLeuLeuArgGlyThrProGlyProSe     461

1326  GCAGGACGGCGTCCGGTGTCAGCACCAGCAGCGGGAGCAGATGAAGGTGT  1375
      |::::::::||||||||||||||  :::::::  ||||||:  :::|||||
461  rLysGluValLeuArgValValGlyValGluProValLysAlaP       478

1376  ACAAGTGCGAACACTGCCGGGTGCTCTTCCTGGATCACGTCATGTACACC  1425
       :||||||||||||||||||||||||||||||||||||||::::||||:
478  heLysCysGluHisCysArgIleLeuPheLeuAspHisValMetPheThr  494

1426  ATCCACATGGCTGCCACGCCTTCCGTGATCCTTTTGAGTGCAACATGTG  1475
      ||||||||||||||||||||||||||||||||||||||||:::::||||
495  IleHisMetGlyCysHisGlyPheArgAspProPheGluCysAsnIleCy  511

1476  CGGCTACCACGCCAGGACGACCGGTACGAGTTCTCGTCGCACATAACGCCGAG 1525
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511  sGlyTyrHisSerGlnAspArgTyrGluPheSerSerHisIleValArgG  528

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528  lyGluHisLys  531
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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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GN   AIOLOS.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
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RN   [1]
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RC   STRAIN=RPL1; TISSUE=BURSA OF FABRICIUS, AND THYMUS;
RX   MEDLINE=99438020; PubMed=10508239;
RA   Liippo J.P., Mansikka A., Lassila O.;
RT   "The evolutionarily conserved avian Aiolos gene encodes alternative
RT   isoforms.";
RL   Eur. J. Immunol. 29:2651-2657(1999).
DR   EMBL; AJ005933; CAB56282.1; -.
DR   HSSP; P15822; 1BBO.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 5.
DR   SMART; SM00355; ZnF_C2H2; 6.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   DNA-binding; Zinc-finger.
SQ   SEQUENCE 494 AA; 55516 MW; 8D3AC945EDB31751 CRC64:

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alignment_scores:
         Quality:  1260.00                Length:    539
         Ratio:       3.273               Gaps:       15
Percent Similarity:  71.429      Percent Identity:  49.351

alignment_block:
US-08-711-417c-165 x Q9PU55        ..

Align seg 1/1 to: Q9PU55   from: 1  to: 494

25  ATGTCTTTCTCATCAGGGAAGGAAAGCCCCCTGTAAGCGATACTCCAGA  74
     ::|||||::::|||||  :::||||   |||  |||
1   MetAspLeuSerAsnProGlnGlyGlnProLysAlaAla.........   13
```

```
75   TGAGGGCGATGAGCCCATGCCGATCCCTCCCACCACCTGG                          124
     |||||:::|||  ::      ::
14   .GluGlyGlnGluValLeu........GluGluCysAspLeuSerL                    26

125  GAGGACAGCCAAAGCTCCAAGAGTCGACAGAGTCGTGGCCAGTAATGTTAAA             174
     ||||||  :: :: :|||::|||    ::::::::|||
26   ysGlyGlnGluValGluGlyAlaAspAsnVal.....GluGluLeuLys                40

175  GTAGAGACTTCAGAGTGATGAAGAGAATGGCGTGCCTGTGAAATGAATGG               224
     |||||||||||||   |||||||:::::::::
41   GluHisSerGlnSerAsnGlyGlnAlaGlyAlaAspPalValLysValLysSe            57

225  GGAAGAAATGTGCGAGAGATTACCAAGTGCTTGATGCCTCGGGAGAGAAAA              274
     :|||:  :::::|  |||||:|   |||:::|
57   rGluTyrGlyAspPArgGluGluserAlaLeuAsnSer.....GluArgM              72

275  TGAATGGCTCCCACAGGACCAGCAGCTCGGCT..........TTG                    312
     ||||::: :::::::::::|      |||
72   etGluAsnProGluGluSerGluLeuProTyrAlaTyrProArgGluTyr              88

313  TCGGGAGTTGGAGGCATTCGACTT..........................               336
     |||
89   SerGluTyrGluGlyIleLysGluLeuGluArgHisLeuGlySerTyrAspSe           105

337  ..........CCTAACGGAAAACTAAAGTGTGATATCTGTGGGATCATTT              376
              ::||||||::   |||||::::|   |  |||||||||:
105  rAlaArgProAlaSerGlyLysMetThrCysAspValCysGlyLeuAlaC             122

377  GCATCGGCGCCCAATGTGCTCATGGTTCACAAAAGAAGCCACACTGGAGAA            426
     |||||:::  |||||||||||||||||||||||||||||||||||
122  ysIleSerLeuAsnValLeuMetValHisLysSArgSerHisThrGlyGlu           138

427  CGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAA             476
     ::||||||:   |||      :::|||||||||||||||||||||
139  ArgProPheGlnCysAsnGlnCysGlyAlaSerPheThrGlnLysGlyAs            155

477  CCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCC             526
     ||||||||||||||||:::|||||||||:::|||||||||||||||||
155  nLeuLeuArgHisIleLysLeuHisThrGlyGluLysProPheLysCysH            172

527  ACCTCTGCAACTACGCCTGCCGCCGGAGGACGACCCTCACTGGCCACCTG             576
     |||||||:   :::|||||:::|||||||||||||:|||||||
172  lsLeuCysSerTyrAlaCysArgArgArgAspAlaLeuThrGlyHisLeu            188

577  AGGACGCCACTCCGTTGGTAAACCTCACAAATGTGGATATTGTGGCCGAAG            626
     |||||||||||||||   ||||| ||||::|||||||||||||||
189  ArgThrHisSerValGluLysProTyrLysCysGluPheCysGlyLysSe            205

627  CTATAAAACAGCGAACGTCTTTAGAGGAACATAAAGAGCGCTGCCACAACT            676
     |||||||||||:::||||||||  ::||||||||||:::::::|
205  rTyrLysGlnArgSerLeuGluGluHisLysGluArgCysArgThrT              222

677  ACTTGGAAAGCATGGGC.......CTTCCGGGCACACTGTACCCAGTCATT           720
     :::::::|||  ::: ||||||::|||::||
222  yrLeuGlnSerThrGlyGlyTyrGlyCysGluProAlaAsnVal.........         234

721  AAGAAGAAAACTAAGCACAGCAGACACCTGTCAAGATAGG                        770
     |||:::::||| :::
235  ......GluAlaArgHisIleLys...........AlaGluMetGl                  244

771  ATCAGAGAGATCTCCGTCTGGACAGACTAGCAAGTAATGTCGCCAAAC               820
     |::||||||||||||||||||||||||||||||||||||:
244  yThrGluArgAlaLeuValLeuAspArgLeuAlaSerAsnValAlaLysA            261

821  GTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGGGCCTGTCC...             867
     |||||||||   |||||::::|||  ||
261  rgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuSerPhe           277

868  GACACCGCCCTACGACAGTGCC...ACGTACGAGAAGGAGAACGAAATGAT           914
     |||::: |||::|   ::::||||||||||||||||||||
278  AspValAsnTyrAsnSerSerPheValTyrGluLysGluGluAspIleVa           294


915  GAAGTCCCACGTGATGGACCAAGCCATCAACAACACGCCATCAACTACCTGG            964
     :::::::|||||||||||||||||||||||||||::|::|||
294  lGlnGlyArgMetMetAspGlnAlaIleAsnAsnAlaIleSerPheLeuG             311

965  GGGCCGAGTCCCTGCGCCCGGTGCAGAGCCCGAGAGCGCCCCCCGGGC...GGTTCC     1011
     |||||||||||||||||||||||||||||||||||||::   :::
311  lyAlaGluAlaLeuArgProLeuValGlnThrProProAlaProAlaPro           327

1012 GAGGTGGTCCGTCATCACGACCGGATGTACCAGCTGCACAGGCGGCTCCGA           1061
     ||||:::|||||||||||||||||||||   :::
328  GluMetValProValIleSerProLeuTyrProIleAlaLeuProArgAl          344

1062 GGGCACCCCGGCGTCCAACCACTCGGCCCCAGGACAGCGCCGTGGAGTACC          1111
     :::||:::::::||
344  aAspValProAsnGlyGlyAsp....................                    351

1112 TGCTGCTCCTCCAAGGCCAAGTTGGTCCCTCGGAGCGCGAGGCGTCC             1161
     |||:::  :::  ||||||||||||||||||||||||:
352  ..........GluLysSerHisValProLeuArgGluArgGluAlaLeuSer         364

1162 CCGAGCAACAGCTGCCAAGACTCCACGGACACCACCGAGAGCAACAACGAGGA        1211
     |||:||||||   :::::|||||||||::|||||||
365  ProAsnAsnSerGlyHisAspSerThrAspSerAsnHisGluGl                 381

1212 GCAG.............................................CGCA        1219
     |:::                                            |||
381  uArgProAsnProProPheProGlnGlyProValLeuProValProArgA          398

1220 GCGGTCTTATCTACCTGACCAACCACCATCGCCCGACGCCGCCAACCGCGTG         1269
     ::|||
398  snGlyLeu.........................................Pro         401

1270 TCGCTCAAGGAGGAGCACCGGCCTACGACCTGCTCGCCGCGCCTCCGA            1319
     ::||||||||   |||         :::::::::::
402  AlaLeuLysAspPheProArgPheAspIleIleLysProProAlaMe            418

1320 GAACTCGCAGGACGACGCCTCCGGTGGTCAGCACCAGCGGGGAGCAGATGA          1369
     :|||||||||||  ::|||||   :::||||||
418  tCysProArgAspAlaPheLysValIleAsnLysAspGlyGluAlaIleG          435

1370 AGGTGTACAAGTGCGAACACTGCCGGGTGCTCTTCCTGGATCAGTCATG           1419
     ::|||||||||||||||||||||||||||||||||::||||
435  lyAlaTyrArgCysAspHisCysArgValLeuPheLeuAspTyrValMet         451

1420 TACACCATCCACATGGGCTGCCACACGGTTCCGTGATCTTTTGAGTGCAA          1469
     :::|||||||||||||||||||||||||||||||||||||||||
452  PheThrIleHisMetGlyCysHisGlyPheArgAspProPheGluCysAs         468

1470 CATGTGCGGCTACCAGCCAGGACGGTACGAGTTCTCGTCGCACATAA            1519
     |:::||||||||||||||||||||||||||||||||||||||||||||
468  nValCysGlyTyrArgSerHisSerAspArgTyrGluPheSerSerHisIleA      485

1520 CGCGAGGGGAGCACCGC                                            1536
     ::|||||||||||||
485  laArgGlyGluHisArg                                            490
```

RT   "Eos and Pegasus, Two Members of the Ikaros Family of Proteins with
RT   Distinct DNA Binding Activities.";
RL   J. Biol. Chem. 275:38347-38354(2000).
DR   EMBL; AF230809; AAG39221.1; -.
DR   HSSP; P15822; 1BBO.
DR   InterPro; IPR000822; Znf-C2H2.
DR   Pfam; PF00096; zf-C2H2; 6.
DR   SMART; SM00355; ZnF_C2H2; 6.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   DNA-binding; zinc-finger.
SQ   SEQUENCE   483 AA;   53219 MW;   C30B0270709C34F9 CRC64;

alignment_scores:
          Quality: 1252.50   Length: 500
          Ratio: 3.528   Gaps: 15
Percent Similarity: 71.000   Percent Identity: 52.400

alignment_block:
US-08-711-417C-165 x Q9H2S9   ..

Align seg 1/1 to: Q9H2S9   from: 1 to: 483

187 AGTGATGAAGAGAATGGG.....................CGTGCCTGTGA 215
        ||||||||||||:::::: || ||
  3 SerAspGluSerSerArgLeuLeuGlyProAspGluArgLeuLeuGl   19

216 AATGAATGGGGAAGAAATGTGCGGAGGAT...............TTACGAA 250
     |||||||||::::|||||||||| ||
 19 uLysAspAspSerVallleValGluAspSerLeuSerGluProLeuGlyT   36

251 TGCTTGATGCCTCGGGAGAGAAAATGAATGAGCTCCCACGGGACCAAGGC 300
        |||::|||| ||| ::::: |||||||||||
 36 yrCysAspGlySerGlyProLysProHisSerPro............   47

301 AGCTCGGCTTTGTCGGGAGTTGAGGCATTCGACTTCCTAACGGAAAACT 350
                 ||||||||||||||||||||||||||||||
 48 ....GlyGlyIleArgLeuProAsnGlyLysLysLe   57

351 AAAGTGTGATATCTGTGGATCATTGCATCGGGCCCCAATGTGCTCATGG 400
     ||||||||::||||||||||||::||||||||||||||||||||
 57 uLysCysAspValCysGlyMetValCysIleGlyProAsnValLeuMetV   74

401 TTCACAAAGAAGCCACACTGAGACAGCGGCCCTTCCAGTGCAATCAGTGC 450
     ||||||||||||||||||||||||||||||:||:||||||||||||
 74 alHisLysArgSerHisThrGlyGluArgProHisCysAsnGlnCys   90

451 GGGGCCTCATTCACCCAGAAGGGCAACCTGCTCCGGCCACATCAAGCTGCA 500
     |||||||||||||||||||||||||||||||||||||||
 91 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 107

501 TTCCGGGAGAAGCCCTCAAATGCCACCTACGGCCTGCCGCC 550
     ||||||||||||| :::||||||||||||||||
107 sSerGlyValCysProPheLysProCysAsnTyrAlaCysArgA 124

551 GGAGGACGGCCCTCACTGGCCACCTGAGGACGCACTCC........... 588
     ||||||||||||||||||||||||||||||
124 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValSerPro 140

589 ...GTTGGTAAACCTCACAAATGTGGATATTGTGGCGAAGCCATAAACA 635
        |||||||::|||||||||||||||
141 ThrValGlyTyrLysProTyrLysCysAsnTyrCysGlyArgSerTyrLysGly 157

636 GCGAACGTCTTTAGAGGAACATAAAGAGCCTGCCAACTACTTGGAAA 685
     |::||||||||||||||||||||||||||||:::|
157 nGlnSerThrLeuGluGluHisLysLysGluArgCysHisLysAsnTyrLeuGlnS 174

686 GCATG.................GGCCTTCCGGCACACTGTAC 711
     |:::: ||| ||||||
174 erLeuSerThrGluAlaGlnAlaLeuAlaLeuGlyGlnProGly......... 187

712 CCAGTCATTAAAGAAGAAGAAACTAAGCACAGTGAAATGGCACAGAAGAC...CT 758

188 ....AspGluIleArgAspLeuGluMetValProAspSerMe 200

759 GTGCAAGATAGGATCAGAGAGATCTTCGTGCTGACAGACTAGCAAGTA 808
        ||||||||||::: ::||||||||||||:::
200 tLeuHisSerSerGluArgAlaThrPheIleAspArgLeuAlaAsnS 217

809 ATGTCGCCAAAGTAGAGCTCTATGCCTCAGAAATTCTTGGGACAAG 858
     ||||||||||||||||::::|||||||||||||||::||:||
217 erLeuThrLysArgLysArgSerThrProGlnLysPheValGlyLysLys 233

859 .......GGCCTGTCCGACACGCCCTACGAC......AGTCCCAC 890
             :::|||||||| ||||||| |||::
234 GlnMetArgPheSerLeuSerAspLeuProTyrAspValAsnSerGlyGl 250

891 GTACGAGAAGGAGAACCAAATGATGAAGTCCCACGTGATGACCAAGCCA 940
     ||||||||||::: ||:::::: |||| :::: ::::
250 yTyrGluLysAspValGlyLeuValGlyHisHisSerLeuGluProGlyP 267

941 TCAACAACGCCATCAACTACCTGGGGGCCGAGTCCCTGCCCCGCTGGTG 990
     :::||||||||||||||||||||||||||||||||||||||||
267 heGlySerSerLeuAlaPheValGlyAlaGluHisLeuArgProLeu... 282

991 CAGAGCGCCCCGGGCGGT.......TCCGAGGTGGTCCCGGTCATCAGCCC 1034
     ::: |||||||||||| ||||||||
283 ArgLeuProProThrHisCysIleSerSerGluLeuThrProValIleSerSe 299

1035 GATGTAC............CAGCTGCACAGGCGCTCGGAG......GGCA 1066
     :::||| || |||||||||||
299 rValTyrThrGlnMetGlnProLeuProGlyArgLeuGluLeuProGlyS 316

1067 CCCCGGCTCCAACCACTCGGCCCAGCACAGCCCGTGGAGTACCTGCTG 1116
     :: |||||||||||:::|| :::||| ::::
316 erArgGluAlaGlyGlyProGluAspLeuAla...AspGlyGlyPro 331

1117 CTGCTCTCCAAGGCCAAGTTGGTGCCCTCGGACGCGCGAGGGTCCCCGAG 1166
     |||||| |||||||||||||||||||
332 LeuLeuTyrArgProArgGlyProLeuThrArgProGlyAlaSerProSe 348

1167 CAACAGCTGCCAAGACTCCACGGACACCGAGAGCAACAAGGAGGAGCAGC 1216
     |||||||||||||| :::|||||||||||||
348 rAsnGlyCysGlnAspSerThrAspThrGluSerAsnHisGluAspArgV 365

1217 GCAGGCGGTCTTATCTACCTG...................... 1236
     ::||||||||||||||||
365 alAlaGlyValValSerLeuProGlnGlyProProGlnProProProPro 381

1237 ACCAACACCATCGCCGACGCGGCCCAACCGCGTGCGCTCAAGGAGGAGCA 1286
     ||| :::||:||| ::: |||||||||||||
382 ThrIleValGlyValArgHisSerProAlaThrAlaLysGluAspProLy 398

1287 CCCGCGCTACGACCTGTCGCGCCGCCTCCGAGAACTCCGACGACGCCGGC 1336
     ||||||||||||||||||||||||||||||||||||||||||
398 sProGlnGluGlyLeuLeuArgGlyThrProGlyProSerLysGluValL 415

1337 TCCGGTGGTGTCAGGCACCACGGGGAGCAGAGTGAAGGTGTACAAGTGCGAA 1386
     |||||||||| ||| ||||||||||||||||
415 euArgValValGlyValGlySerSerGluProValAlaGluLysCysGlu 431

1387 CACTGCGCGGGTGCTTCTTCCTGGATCACGTCATGTACCACCCATCACATGG 1436
     ||||||||||:||:|||||||||||::: ||||||||||||||
432 HisCysArgIleLeuPheLeuAspHisValMetPheThrIleHisMetGl 448

1437 CTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTCGGCTACCACA 1486
     ||||||||||||||||:::||||||||||||||||||||||||||
448 yCysHisGlyPheArgAspProPheGluCysAsnIleCysGlyTyrHisS 465

1487 GCCAGGACCGGTACGAGTTCTCGCACATAACGCGAGGGAGCACCGGC 1536
     ||||||||||||||||||||||||||||||||||||||||||
465 erGlnAspArgTyrGluPheSerHisIleValArgGlyHisHisLys 481

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